GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 15:11:57 ; Search time 3229.12 Seconds
(without alignments)
10265.033 Million cell updates/sec

Title: US-10-070-532-3
Perfect score: 1110
Sequence: 1 atggagccctcagccacccc.....ttccctggagtctgctctaa 1110

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*

28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	729.2	65.7	1740	11	BC035686	BC035686 Homo sapi
c	2	696	62.7	886	13	BX433093	BX433093 BX433093
c	3	650.4	58.6	899	13	BX433092	BX433092 BX433092
	4	554.4	49.9	753	29	AY420885	AY420885 Homo sapi
	5	521.4	47.0	3470	11	AK048781	AK048781 Mus muscu
	6	521.4	47.0	3729	11	AK038551	AK038551 Mus muscu
	7	511.8	46.1	1790	11	BC035858	BC035858 Homo sapi
	8	510.4	46.0	3153	11	AK079572	AK079572 Mus muscu
c	9	500.6	45.1	790	14	CF147830	CF147830 AGENCOURT
	10	467.2	42.1	750	29	AY420886	AY420886 Pan trogl
	11	462.4	41.7	726	29	AY420887	AY420887 Mus muscu
	12	462.4	41.7	1001	9	AL535838	AL535838 AL535838
	13	385.2	34.7	993	12	BM926746	BM926746 AGENCOURT
	14	376.2	33.9	543	13	BX119589	BX119589 BX119589
	15	359	32.3	788	14	CF147829	CF147829 AGENCOURT
	16	322.8	29.1	382	12	BQ042116	BQ042116 sheep1 Sh
c	17	288	25.9	525	12	BI133700	BI133700 UI-M-BH3-
	18	280.6	25.3	635	12	BM939496	BM939496 UI-M-BH3-
	19	277.8	25.0	520	13	BQ269289	BQ269289 ik23f12.y
	20	264.2	23.8	627	10	BB632359	BB632359 BB632359
	21	263.8	23.8	599	12	BM933820	BM933820 UI-M-BH3-
	22	261.6	23.6	611	13	BY723922	BY723922 BY723922
	23	248.4	22.4	892	13	BX409735	BX409735 BX409735
	24	208.8	18.8	477	12	BM087401	BM087401 500158 MA
	25	200.8	18.1	662	10	BB632883	BB632883 BB632883
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	28	197.6	17.8	505	10	BB651179	BB651179 BB651179
	29	195.2	17.6	245	12	BI976482	BI976482 485407 MA
	30	186.2	16.8	464	13	BY239887	BY239887 BY239887
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c	32	164.2	14.8	703	29	CE375359	CE375359 tigr-gss-
	33	162	14.6	721	29	CE235359	CE235359 tigr-gss-
	34	161.6	14.6	1290	29	AY411591	AY411591 Homo sapi
	35	156.2	14.1	1296	29	AY411593	AY411593 Mus muscu
c	36	155.6	14.0	1013	9	AL535837	AL535837 AL535837
	37	146.2	13.2	768	13	BX109847	BX109847 BX109847
	38	133	12.0	257	10	AW427900	AW427900 64510 MAR
	39	120.2	10.8	526	29	CG978334	CG978334 CH240_169
c	40	119.2	10.7	1005	28	CC212654	CC212654 CH261-75F
c	41	119.2	10.7	1058	28	CC297061	CC297061 CH261-177
	42	117.4	10.6	1113	29	AY420480	AY420480 Homo sapi
	43	115.4	10.4	1100	29	AY420481	AY420481 Pan trogl
c	44	114.4	10.3	1194	28	CC279941	CC279941 CH261-24C
	45	108.8	9.8	1113	29	AY420482	AY420482 Mus muscu

ALIGNMENTS

RESULT 1
BC035686
LOCUS BC035686 1740 bp mRNA linear HTC 20-SEP-2002
DEFINITION Homo sapiens, Similar to hypocretin (orexin) receptor 1, clone IMAGE:5750551, mRNA.
ACCESSION BC035686
VERSION BC035686.1 GI:23242909
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1740)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: http://www.nisc.nih.gov/
Contact: nisc_mgc@nhgri.nih.gov
Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P., Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R., Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C., McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L., Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 79 Row: m Column: 17
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4557636
This clone has the following problem: frame shifted.

FEATURES Location/Qualifiers
source 1. .1740
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5750551"
/tissue_type="Lung, Spleen, fetal, pooled"

/clone_lib="NIH_MGC_122"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 65.7%; Score 729.2; DB 11; Length 1740;
Best Local Similarity 83.2%; Pred. No. 4e-138;
Matches 923; Conservative 0; Mismatches 8; Indels 179; Gaps 1;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        506 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 565

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        566 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 625

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        626 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 685

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        686 CTGGTGGGCAACACGCTG---------------------------------------- 703

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Db        704 ---------------------------------------------------------- 703

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Db        704 ---------------------------------------------------------- 703

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        704 ----------------GGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 746

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        807 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 866

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db        867 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 926

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        927 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 986

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db       1047 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 1106

Qy        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1227 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1286

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1287 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1346

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1347 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1406

Qy       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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Db       1407 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1436
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RESULT 2
BX433093/c
LOCUS       BX433093                886 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX433093 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF013YE04 3-PRIME, mRNA sequence.
ACCESSION   BX433093
VERSION     BX433093.1  GI:30779168
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 886)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 151.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_2&cluster=151.r.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_2.
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FEATURES             Location/Qualifiers
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                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN

  Query Match             62.7%;  Score 696;  DB 13;  Length 886;
  Best Local Similarity   98.5%;  Pred. No. 1.7e-131;
  Matches  702;  Conservative    0;  Mismatches   11;  Indels    0;  Gaps    0;

Qy        377 AGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGT 436
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Db        745 AGGCTGTGTCCGTGTCAGTGACAGTGCTAACTCTCAGCTTCATCGCCCTGGACCGCTGGT 686

Qy        437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC 496
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Db        685 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATNC 626

Qy        497 TGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCA 556
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Db        625 TGGGCATCTGGCCTGTGTCGCTGGCCATCATGGTGCCCAGGGCTGCAGTCATGCAATGCA 566

Qy        557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCT 616
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Db        565 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 506

Qy        617 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 676
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Qy        677 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 736
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Qy        737 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGG 796
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Qy        797 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTG 856
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Db        325 GGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTG 266

Qy        857 AAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGG 916
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Qy        917 TCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGA 976
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Qy       1037 TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGC 1089
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Db         85 TGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGC 33


RESULT 3
BX433092/c
LOCUS       BX433092                899 bp    mRNA    linear   EST 15-MAY-2003
DEFINITION  BX433092 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF013YE04 3-PRIME, mRNA sequence.
ACCESSION   BX433092
VERSION     BX433092.1  GI:30779167
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 899)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 151.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0BAI011ZB01_CS00962_1&cluster=151.r.
            Contact : Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0BAI011ZB01_CS00962_1.
FEATURES             Location/Qualifiers
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                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN

  Query Match             58.6%;  Score 650.4;  DB 13;  Length 899;
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Best Local Similarity 94.0%; Pred. No. 3.5e-122;
Matches 686; Conservative 0; Mismatches 43; Indels 1; Gaps 1;

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              | ||    |||||||    ||||||||||||||  ||||||||||||| ||  |  |||
Db        738 TGTAAGNNCTGTGTCGTGTTCAGTGGCAGTGCTACTTCTCAGCTTCATCGCCTGGACCCG 679

Qy        432 CTGGTATGCCATC-TGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCT 490
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Db        678 CTGGTATGCCATCATCCCACCCACTATTGTCAAAGAGCACAGCCCGGCGGGCCCGTGCTC 619

Qy        491 CCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGC 550
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Db        618 CCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGG 559

Qy        551 AATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATG 610
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Db        558 AATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCAGTCTGTGATG 499

Qy        611 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCT 670
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Db        498 AACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCT 439

Qy        671 ACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGG 730
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Qy        731 GCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACC 790
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Qy        791 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCC 850
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Db        318 AGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCCCGCGCCTTCC 259

Qy        851 TGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 910
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        258 TGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGC 199

Qy        911 TGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 970
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||
Db        198 TGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGT 139

Qy        971 TCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 1030
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 TCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCC 79

Qy       1031 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGGCC 1090
              |||||||||||||||||||||||||||||||||||||||  |  | |  |||
Db         78 ACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTCAACTTCCTCAGGTGCAA 19

Qy       1091 TTCCCTGGAG 1100
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Db         18 ATTCCGGGAG 9
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RESULT 4

AY420885

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LOCUS       AY420885                753 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Homo sapiens HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY420885
VERSION     AY420885.1  GI:39776842
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 753)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 753)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence as made by sequencing genomic exons and ordering them
            based on alignment.
FEATURES             Location/Qualifiers
     source          1. .753
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
     gene            <1. .>753
                     /gene="HCRTR1"
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ORIGIN
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  Query Match             49.9%;  Score 554.4;  DB 29;  Length 753;
  Best Local Similarity   98.9%;  Pred. No. 1.2e-102;
  Matches  558;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy        526 ATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
              ||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||
Db          1 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 60

Qy        586 ACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
              |||||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db         61 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 120

Qy        646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 180

Qy        706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
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Db        181 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 240

Qy        766 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
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Db        241 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 300

Qy        826 CCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
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Db        301 CCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 360

Qy        886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGC 945
                |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        361 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGC 420

Qy        946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 480

Qy       1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
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Db        481 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 540

Qy       1066 ATCATCTACAACTTCCTCAGTGGC 1089
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Db        541 ATCATCTACAACTTCCTCAGTGGC 564
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RESULT 5
AK048781
LOCUS       AK048781               3470 bp    mRNA    linear   HTC 20-SEP-2003
DEFINITION  Mus musculus 0 day neonate cerebellum cDNA, RIKEN full-length
            enriched library, clone:C230065B06 product:OREXIN RECEPTOR TYPE 2,
            full insert sequence.
ACCESSION   AK048781
VERSION     AK048781.1  GI:26339571
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
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Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.

TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

JOURNAL Genome Res. 10 (11), 1757-1771 (2000)

MEDLINE 20530913

PUBMED 11076861

REFERENCE 4

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

TITLE Functional annotation of a full-length mouse cDNA collection

JOURNAL Nature 409, 685-690 (2001)

REFERENCE 5

AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL Nature 420, 563-573 (2002)

REFERENCE 6 (bases 1 to 3470)

AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

TITLE Direct Submission

JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.

FEATURES Location/Qualifiers

source 1. .3470
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:C230065B06"

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                     /db_xref="MGI:2415851"
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                     /dev_stage="0 day neonate"
     CDS             75. .1457
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                     YPKMYHICFFLVTYMAPLCLMILAYLQIFRKLWCRQIPGTSSVVQRKWKQQQPVSQPR
                     GSGQQSKARISAVAAEIKQIRARRKTARMLMVVLLVFAICYLPISILNVLKRVFGMFT
                     HTEDRETVYAWFTFSHWLVYANSAANPIIYNFLSGKFREEFKAAFSCCLGVHHRQGDR
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                     /note="putative"
ORIGIN

  Query Match             47.0%;  Score 521.4;  DB 11;  Length 3470;
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  Matches  712;  Conservative    0;  Mismatches  291;  Indels    6;  Gaps    1;

Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
              | || || || || || || || |||||| | || || ||  |||| ||| | |||||||
Db        178 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTACACCCGAAAGAATATGAGT 237

Qy        140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
              ||||||| ||||||| ||| |    |||||||| ||||| ||  | || |||   ||||
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Qy        200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
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Qy        260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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Db        358 ACCTTTCCCTAGCAGATGTGCTTGTGACCATCACCTGCCTTCCAGCTACCCTCGTTGTTG 417

Qy        320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
              |||||||||||| | ||| | || || ||  ||||||| |||||||| || ||| |||||
Db        418 ACATCACTGAGACTTGGTTCTTTGGACAGTCCCTCTGTAAGGTCATTCCTTATTTACAGA 477

Qy        380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
              ||||||| ||||| ||| | || || ||  | |||| |||  || ||||||| ||||| |
Db        478 CTGTGTCAGTGTCTGTGTCTGTTCTTACGTTGAGCTGCATTGCCTTGGACCGATGGTACG 537
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Qy        440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Db        538 CCATTTGTCACCCTTTGATGTTCAAGAGCACAGCCAAACGGGCTCGAAACAGCATCGTTG 597

Qy        500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
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Db        598 TCATCTGGATCGTCTCCTGCATCATAATGATTCCTCAAGCCATTGTCATGGAGTGCAGCA 657

Qy        560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
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Db        658 GCATGCTCCCTGGCCTAGCCAATAAGACCACCCTCTTTACAGTATGTGATGAACACTGGG 717

Qy        620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
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Db        718 GCGGTGAAGTTTACCCAAAGATGTACCATATCTGCTTCTTTCTGGTGACATACATGGCAC 777

Qy        680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
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Db        778 CTCTGTGTCTTATGATATTGGCTTATCTCCAAATATTCCGTAAACTCTGGTGCCGACAGA 837

Qy        740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
              | ||||| ||  | || |   |   | | || |||||||  |       | ||||  ||
Db        838 TTCCCGGAACTTCTTCTGTGGTTCAGAGAAAATGGAAGCAGC------AGCAGCCGGTTT 891

Qy        800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
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Db        892 CTCAGCCCCGGGGGTCCGGACAGCAGAGCAAGGCTCGGATTAGCGCTGTTGCTGCTGAGA 951

Qy        860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
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Db        952 TAAAGCAGATCCGAGCACGAAGGAAAACAGCCCGGATGCTCATGGTTGTACTTCTGGTCT 1011

Qy        920 TCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
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Db       1012 TTGCAATTTGCTATCTACCAATCAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1071

Qy        980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
              ||   ||  |    ||| | ||  ||||||| || || ||||| || || || ||||| |
Db       1072 TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTTCACTTTTTCTCATTGGCTTG 1131

Qy       1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
              | || |||||||| ||||| ||||| || || || || || || |||||
Db       1132 TATATGCCAACAGTGCTGCAAACCCAATTATTTATAATTTTCTTAGTGG 1180
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RESULT 6
AK038551
LOCUS AK038551 3729 bp mRNA linear HTC 19-SEP-2003
DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230036M08 product:OREXIN RECEPTOR TYPE 2, full insert sequence.
ACCESSION AK038551
VERSION AK038551.1 GI:26332642
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 3729)
AUTHORS Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N., Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,

```
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
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                     /note="putative"
     polyA_site      3729
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ORIGIN

  Query Match             47.0%;  Score 521.4;  DB 11;  Length 3729;
  Best Local Similarity   70.6%;  Pred. No. 1.4e-95;
  Matches  712;  Conservative    0;  Mismatches  291;  Indels    6;  Gaps    1;

Qy          80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
               | || || || || || || || |||||| | || || ||  |||| ||| | |||||||
Db         179 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTACACCCGAAAGAATATGAGT 238

Qy         140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
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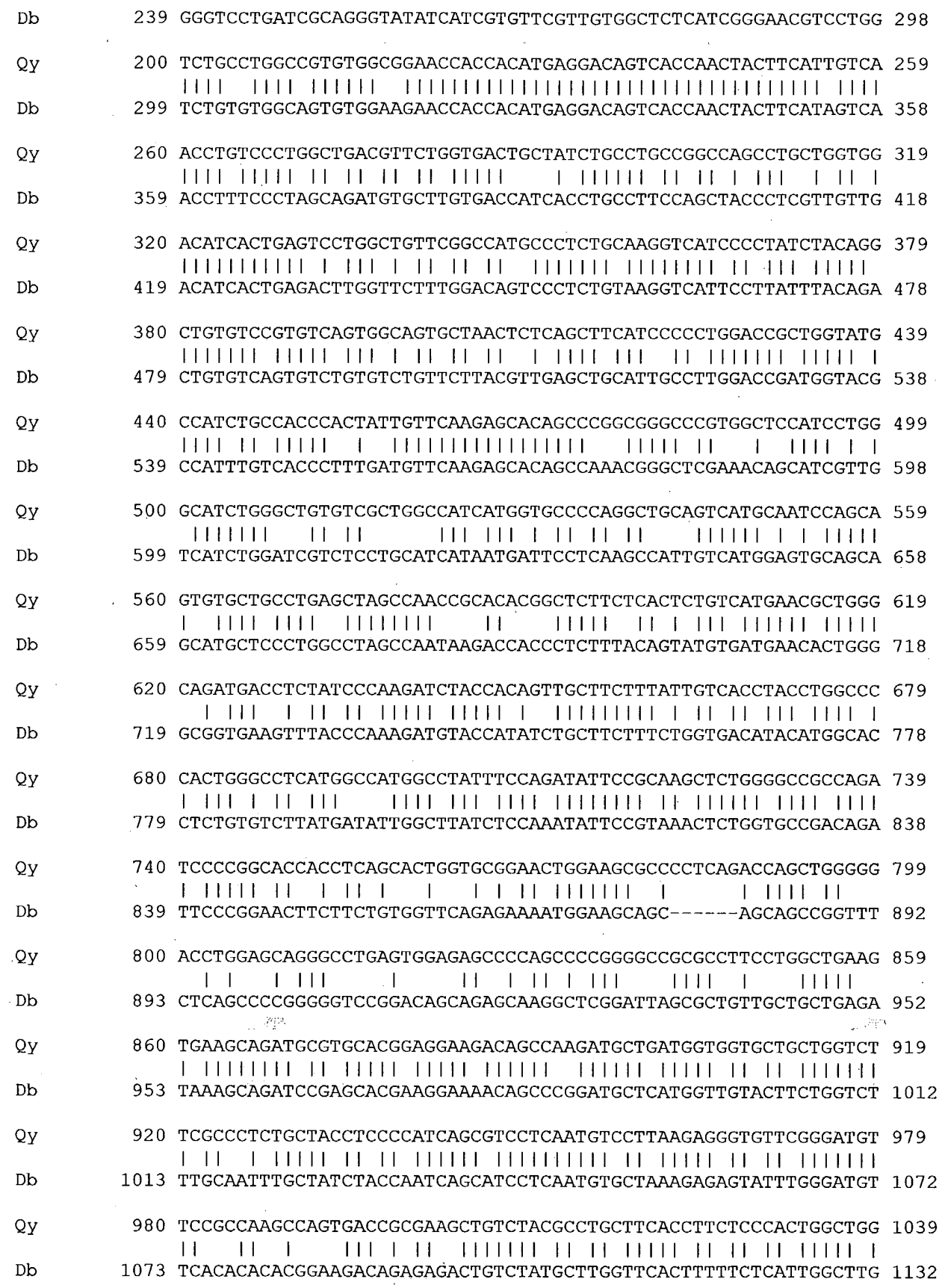

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Qy       1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
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Db       1133 TATATGCCAACAGTGCTGCAAACCCAATTATTTATAATTTTCTTAGTGG 1181
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RESULT 7
BC035858

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LOCUS       BC035858                1790 bp    mRNA    linear   HTC 04-MAR-2003
DEFINITION  Homo sapiens, Similar to hypocretin (orexin) receptor 2, clone
            IMAGE:5767576, mRNA.
ACCESSION   BC035858
VERSION     BC035858.1  GI:23959160
KEYWORDS    HTC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1790)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JUL-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
            cDNA Library Preparation: Life Technologies, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://www.nisc.nih.gov/
            Contact: nisc_mgc@nhgri.nih.gov
            Akhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
            Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
            Dietrich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
            Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
            Maduro,Q.L., Masiello,C., Maskeri,B., Mastrian,S.D.,McCloskey,J.C.,
            McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
            Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
            Young,A., Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 79 Row: p Column: 14
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 6006037
            This clone has the following problem: retained intron.
FEATURES             Location/Qualifiers
     source          1. .1790
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5767576"
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/tissue_type="Brain, fetal, whole pooled"
/clone_lib="NIH_MGC_121"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 46.1%; Score 511.8; DB 11; Length 1790;
Best Local Similarity 70.0%; Pred. No. 9e-94;
Matches 706; Conservative 0; Mismatches 297; Indels 6; Gaps 1;

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Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
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Db        146 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 205

Qy        140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
              ||||||| ||||| |  ||  |    |||||||||||||| ||  | || |||   ||||
Db        206 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 265

Qy        200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
              | ||  |||| ||||||  |||||||||||||||||| || ||||||||||||| ||||
Db        266 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 325

Qy        260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
              | || || ||||||||  || || |||||    | |||||| || ||||  ||| | ||||
Db        326 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 385

Qy        320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
              | |||||||||  ||||| | || || ||  |||| ||||| || || || |||||||||
Db        386 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 445

Qy        380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
              | ||||| ||||| ||| | || || || || ||||  ||| || |||| || |||||||
Db        446 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 505

Qy        440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
              | ||||| ||||| .| |||| ||||||||||   ||||||||||  |  |||  |
Db        506 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 565

Qy        500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
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Db        566 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 625

Qy        560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
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Db        626 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 685

Qy        620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
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Db        686 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 745

Qy        680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
              |||||  | |||||||   |||| ||| | || ||||| ||||| |||||| | || ||||
Db        746 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 805

Qy        740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
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Db        806 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 859
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Qy        800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
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Db        860 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA 919

Qy        860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
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Db        920 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 979

Qy        920 TCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
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Db        980 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1039

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Db       1040 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1099

Qy       1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
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RESULT 8
AK079572

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LOCUS       AK079572                3153 bp    mRNA    linear   HTC 19-SEP-2003
DEFINITION  Mus musculus adult male hypothalamus cDNA, RIKEN full-length
            enriched library, clone:A230091E19 product:OREXIN RECEPTOR TYPE 2,
            full insert sequence.
ACCESSION   AK079572
VERSION     AK079572.1  GI:26348079
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
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  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 3153)
  AUTHORS   Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P.,
            Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hashizume,W.,
            Hayashida,K., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hirozane,T.,
            Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T.,
            Katoh,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M.,
            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M.,
            Nakamura,M., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Ohsato,N.,
            Okazaki,Y., Saito,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N.,
            Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T.,
            Sogabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S.,
            Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A.,
            Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp,
            URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues.
            Please visit our web site for further details.
            URL:http://genome.gsc.riken.go.jp/
            URL:http://fantom.gsc.riken.go.jp/.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="C57BL/6J"
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                     /sex="male"
                     /tissue_type="hypothalamus"
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                     MFKSTAKRARNSIVVIWIVSCIIMIPQAIVMECSSMLPGLANKTTLFTVCDEHWGGEV
                     YPKMYHICFFLVTYMAPLFLMILAYLQIFRKLWCRQIPGTSSVVQRKWKQQQPVSQPR
                     GSGQQSKARVSAVAAEIKQIRARRKTARMLMVVLLVFAICYLPISILNVLKRVFGMFT
                     HTEDRETVYAWFTFPHWLVYANSCCKPNYL"
ORIGIN

  Query Match          46.0%;  Score 510.4;  DB 11;  Length 3153;
  Best Local Similarity  70.5%;  Pred. No. 2.2e-93;
  Matches  712;  Conservative    0;  Mismatches  291;  Indels    7;  Gaps    2;

Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
              | || || || || || || || |||||| | || || ||  |||| ||| | |||||||
Db        211 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTACACCCGAAAGAATATGAGT 270

Qy        140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
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Db        271 GGGTCCTGATCGCAGGGTATATCATCGTGTTCGTTGTGGCTCTCATCGGGAACGTCCTGG 330

Qy        200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
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Db        331 TCTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACAGTCACCAACTACTTCATAGTCA 390

Qy        260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
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Db        391 ACCTTTCCCTAGCAGATGTGCTTGTGACCATCACCTGCCTTCCAGCTACCCTCGTTGTTG 450

Qy        320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
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Qy        380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
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Qy        440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Qy        500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
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Db        631 TCATCTGGATCGTCTCCTGCATCATAATGATTCCTCAAGCCATTGTCATGGAGTGCAGCA 690

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Qy        620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
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Db        811 CTCTGTTTCTTATGATATTGGCTTATCTCCAAATATTCCGTAAACTCTGGTGCCGACAGA 870

Qy        740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
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Db        871 TTCCCGGAACTTCTTCTGTGGTTCAGAGAAAATGGAAGCAGC------AGCAGCCGGTTT 924

Qy        800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
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Qy        860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
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Db        985 TAAAGCAGATCCGAGCACGAAGGAAAACAGCCCGGATGCTCATGGTTGTACTTCTGGTCT 1044

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Qy        980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
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Db       1105 TCACACACACGGAAGACAGAGAGACTGTCTATGCTTGGTTCACTTTTCCTCATTGGCTTG 1164

Qy       1040 TGTACGCCAACAGC-GCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
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Db       1165 TATATGCCAACAGCTGCTGCAAACCCAATTATTTATAATTTTCTTAGTGG 1214
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RESULT 9
CF147830/c
LOCUS       CF147830                790 bp    mRNA    linear   EST 25-JUL-2003
DEFINITION  AGENCOURT_14740202 NIH_MGC_145 Homo sapiens cDNA clone
            IMAGE:6971889 5', mRNA sequence.
ACCESSION   CF147830
VERSION     CF147830.1  GI:33244098
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 790)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: GPCR Consortium
            cDNA Library Preparation: GPCR Consortium
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRBI02 row: a column: 08
High quality sequence start: 7
High quality sequence stop: 738.

FEATURES Location/Qualifiers
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/note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2: varies by clone; ORFs were PCR-amplified and cloned into pcDNA3.1 by the GPCR Consortium. Cloning sites vary by clone and include the following: 5'-EcoRV-XmnI/XhoI-3', 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional). For information about which gene each clones represents, please visit our anonymous ftp site at ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.data Note: this is a NIH_MGC Library."

ORIGIN

Query Match 45.1%; Score 500.6; DB 14; Length 790;
Best Local Similarity 99.2%; Pred. No. 1.2e-91;
Matches 503; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy        583 CGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATC 642
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Qy        643 TACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 702
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        730 TACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCC 671

Qy        703 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 762
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        670 TATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTG 611

Qy        763 GTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 822
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        610 GTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGA 551

Qy        823 GAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG 882
              ||||||||||||||| ||||||||||||||||||||||||||||||||||||||||||||
Db        550 GAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGG 491

Qy        883 AAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATC 942
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db        490 AAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATC 431

Qy        943 AGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 1002
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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         430 AGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAA 371

Qy        1003 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 1062
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         370 GCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAAC 311

Qy        1063 CCCATCATCTACAACTTCCTCAGTGGC 1089
                |||||||||||||||||||||||||||
Db         310 CCCATCATCTACAACTTCCTCAGTGGC 284


RESULT 10
AY420886
LOCUS       AY420886                750 bp    DNA     linear   GSS 17-DEC-2003
DEFINITION  Pan troglodytes HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence,
            genomic survey sequence.
ACCESSION   AY420886
VERSION     AY420886.1  GI:39776843
KEYWORDS    GSS.
SOURCE      Pan troglodytes (chimpanzee)
  ORGANISM  Pan troglodytes
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE   1  (bases 1 to 750)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 750)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence as made by sequencing genomic exons and ordering them
            based on alignment.
FEATURES             Location/Qualifiers
     source          1. .750
                     /organism="Pan troglodytes"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9598"
     gene            <1. .>750
                     /gene="HCRTR1"
                     /locus_tag="HCM7373"
ORIGIN

  Query Match             42.1%;  Score 467.2;  DB 29;  Length 750;
  Best Local Similarity   83.7%;  Pred. No. 7.6e-85;
  Matches  472;  Conservative    0;  Mismatches   92;  Indels    0;  Gaps    0;
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Qy        526 ATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
              ||||||||||||||||||||||| ||| ||||||||||||||||||||||||||||||||
Db          1 ATGGTGCCCCAGGCTGCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 60

Qy        586 ACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
              ||||||||||||||| ||||| ||||||||||||||||||||||||||||||||||||||
Db         61 ACACGGCTCTTCTCAGTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 120

Qy        646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 180

Qy        706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 240

Qy        766 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 300

Qy        826 CCCCAGCCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
              |||||||||||||| ||||||||||||||||||||||||||||||||| |||||||||
Db        301 CCCCAGCCCCCGGGCCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCGCGGAGGAAG 360

Qy        886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGC 945
              |||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db        361 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGT 420

Qy        946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
              ||||||||||||||||||||
Db        421 GTCCTCAATGTCCTTAAGAGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 480

Qy       1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
                                                 ||||||||||    |||||||||
Db        481 NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNACGCCAACAGNNNNGCCAACCCC 540

Qy       1066 ATCATCTACAACTTCCTCAGTGGC 1089
              ||||   ||||||||||||||||
Db        541 ATCANNNACAACTTCCTCAGTGGC 564
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RESULT 11
AY420887
LOCUS AY420887 726 bp DNA linear GSS 17-DEC-2003
DEFINITION Mus musculus HCRTR1 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.
ACCESSION AY420887
VERSION AY420887.1 GI:39776844
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 726)
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A., Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B., Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,

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            Adams,M.D. and Cargill,M.
  TITLE     Inferring nonneutral evolution from human-chimp-mouse orthologous
            gene trios
  JOURNAL   Science 302 (5652), 1960-1963 (2003)
   PUBMED   14671302
REFERENCE   2  (bases 1 to 726)
  AUTHORS   Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejariwal,A.,
            Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,
            Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Sninsky,J.J.,
            Adams,M.D. and Cargill,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
            Rockville, MD 20850, USA
COMMENT     This sequence as made by sequencing genomic exons and ordering them
            based on alignment.
FEATURES             Location/Qualifiers
     source          1. .726
                     /organism="Mus musculus"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:10090"
     gene            <1. .>726
                     /gene="HCRTR1"
                     /locus_tag="HCM7373"
ORIGIN

  Query Match             41.7%;  Score 462.4;  DB 29;  Length 726;
  Best Local Similarity   87.0%;  Pred. No. 7.2e-84;
  Matches  508;  Conservative    0;  Mismatches   76;  Indels    0;  Gaps    0;

Qy        526 ATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGC 585
              ||||||||||||||||| |||||| | | |||||| |||||||||||||||||||| |||
Db          1 ATGGTGCCCCAGGCTGCTGTCATGGAGTGCAGCAGCGTGCTGCCTGAGCTAGCCAATCGC 60

Qy        586 ACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTAC 645
              || |||||||||||  ||||| |||| | ||||||||||| ||||| ||||||||||||
Db         61 ACCCGGCTCTTCTCTGTCTGTGATGAGCACTGGGCAGATGAACTCTACCCCAAGATCTAT 120

Qy        646 CACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTAT 705
              ||||| ||||| || ||||||||||||||||||||||||||||||||||| |||||||||
Db        121 CACAGCTGCTTTTTCATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCTATGGCCTAT 180

Qy        706 TTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTG 765
              |||||||| |||||||||||||||||||||||||||| || ||||| ||||| |||||
Db        181 TTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCTGGTACCACATCAGCCTTGGTG 240

Qy        766 CGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAG 825
              |||||||||| || ||||| || || |||| ||  | | | |||||||| ||  ||||
Db        241 CGGAACTGGAAACGGCCCTCGGAACAACTGGAGGCTCAGCACCAGGGCCTCTGTACAGAG 300

Qy        826 CCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAG 885
              |||||||||||| ||| |||||||||||||| |||||||||||||| || |||||||||
Db        301 CCCCAGCCCCGGGCCCGAGCCTTCCTGGCTGAGGTGAAGCAGATGCGAGCTCGGAGGAAG 360

Qy        886 ACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGC 945
              || || |||||||||||||| || |||||||| || || ||||| || || ||||||||
Db        361 ACGGCTAAGATGCTGATGGTAGTCCTGCTGGTTTTTGCACTCTGTTATCTGCCCATCAGT 420
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Qy        946 GTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCT 1005
              ||||||||||||||||||| |||||||||||||||||||||| ||||| |||||
Db        421 GTCCTCAATGTCCTTAAGAGAGTGTTCGGGATGTTCCGCCAAGCCAGCGACCGGGAAGCC 480

Qy       1006 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCC 1065
              |||||||||||||||||||||||||||||| |||||||||||| || ||||||||
Db        481 GTCTACGCCTGCTTCACCTTCTCCCACTGGCTAGTGTACGCCAACAGTGCCGCCAACCCT 540

Qy       1066 ATCATCTACAACTTCCTCAGTGGCCTTCCCTGGAGTCTGCTCTA 1109
              ||||||||||||||||||||||     | ||   | | || |
Db        541 ATCATCTACAACTTCCTCAGTGGCAAATTCCGGGAGCAGTTCAA 584


RESULT 12
AL535838
LOCUS       AL535838               1001 bp    mRNA    linear   EST 12-MAY-2003
DEFINITION  AL535838 Homo sapiens FETAL BRAIN Homo sapiens cDNA clone
            CS0DF013YE04 5-PRIME, mRNA sequence.
ACCESSION   AL535838
VERSION     AL535838.2  GI:30542758
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1001)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 13, 2001 this sequence version replaced gi:12799331.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 151.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DF013BC02QP1&cluster=151.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DF013BC02QP1.
FEATURES             Location/Qualifiers
     source          1. .1001
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DF013YE04"
                     /tissue_type="FETAL BRAIN"
                     /dev_stage="fetal"
                     /clone_lib="Homo sapiens FETAL BRAIN"
                     /note="Organ: brain; Vector: pCMVSPORT_6; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime end
                     enriched, double-strand cDNA was digested with Not I and
                     cloned into the Not I and EcoRV sites of the pCMVSPORT 6
                     vector. Library was not normalized."
ORIGIN
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  Query Match             41.7%;  Score 462.4;  DB 9;  Length 1001;
  Best Local Similarity   91.0%;  Pred. No. 8.3e-84;
  Matches  538;  Conservative   13;  Mismatches   31;  Indels    9;  Gaps    6;

Qy        377 AGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGT 436
              |||||||||||||||| ||||||||||||||:| ||||||| |:||||||||||||
Db        415 AGGCTGTGTCCGTGTCANTGGCAGTGCTAACTCTMANCTTCATCGCMCTGGACCGCTGGT 474

Qy        437 ATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCC 496
              ||||:||||||:||||||||||||||||||:|||||||||||||||||||||||||||||
Db        475 ATGCHATCTGCYACCCACTATTGTTCAAGARCACAGCCCGGCGGGCCCGTGGCTCCATCC 534

Qy        497 TGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCA 556
              |  | ||||||||| | ||||||||||||||||||||||||||||||||||| ||| ||
Db        535 TNNGNATCTGGGCTNTNTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGGAATGCA 594

Qy        557 GCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCT 616
              |||||||||||||| ||||| |||||||||||||||||||||| ||||| |||||||||
Db        595 GCAGTGTGCTGCCTNAGCTANCCAACCGCACACGGCTCTTCTCAGTCTGTGATGAACGCT 654

Qy        617 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 676
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        655 GGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGG 714

Qy        677 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 736
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        715 CCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCC 774

Qy        737 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCT-G 795
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        775 AGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGG 834

Qy        796 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCT 855
              |||||||||||||||||||||||||||||||     ||| ||||||||||||||||||
Db        835 GGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCC--AGCCCCGGGCCGCGCCTTCCTGGCT 892

Qy        856 GAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTG 915
              |||||||   : |   |      ||  |:||||:|:|||||||||||||||:|||||||
Db        893 GAAGTGA---RCAGATGSTGCAGGCAGVAGACASCSAAGATGCTGATGGTGGBGCTGCTG 949

Qy        916 GTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGG 966
              :|||||| ||||||||||:|  |||||||:|| |||||||| | ||||||
Db        950 STCTTCG-CCTCTGCTACST-GCCATCAGSGT-CTCAATGTCTTAAAGAGG 997


RESULT 13
BM926746
LOCUS       BM926746                993 bp    mRNA    linear   EST 12-MAR-2002
DEFINITION  AGENCOURT_6681991 NIH_MGC_121 Homo sapiens cDNA clone IMAGE:5767576
            5', mRNA sequence.
ACCESSION   BM926746
VERSION     BM926746.1  GI:19377125
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Life Technologies, Inc.
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM12826  row: a  column: 17
            High quality sequence stop: 684.
FEATURES             Location/Qualifiers
     source          1. .993
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5767576"
                     /lab_host="DH10B"
                     /clone_lib="NIH_MGC_121"
                     /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: EcoRV (destroyed); RNA source anonymous pool of 3
                     fetal brains, female age 20 weeks, female age 24 weeks,
                     and male age 26 weeks.  Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed  upon
                     cloning).  Average insert size 1.7 kb, insert size range
                     0.7-3.5 kb.  Library is normalized and enriched for
                     full-length clones and  was constructed by C. Gruber
                     (Invitrogen).  Research Genetics  tracking code 017. Note:
                     this is a NIH_MGC Library."
ORIGIN

  Query Match             34.7%;  Score 385.2;  DB 12;  Length 993;
  Best Local Similarity   71.4%;  Pred. No. 4.6e-68;
  Matches  507;  Conservative    0;  Mismatches  203;  Indels    0;  Gaps    0;

Qy          80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
               | || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db         145 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 204

Qy         140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
               ||||||| ||||| |  ||  |    ||||||||||||| ||  | || |||   ||||
Db         205 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 264

Qy         200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
               | ||  |||| ||||||  ||||||||||||||||| || ||||||||||||| ||||
Db         265 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 324

Qy         260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
               | || || |||||||| || || |||||    | |||||| || ||||  ||| | ||||
Db         325 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 384

Qy         320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
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                | ||||||||| ||||| | || || ||  |||| ||||| || || || |||||||||
Db        385 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 444

Qy        380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
                | ||||| ||||| ||| | || || || || ||||  ||| || |||| || |||||||
Db        445 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 504

Qy        440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
                | ||||| |||||  |  |||| ||||||||||   |||||||||  |  |||  |
Db        505 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 564

Qy        500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
                |||||||  ||| ||       || ||| | || |||||    |||||| | | |||||
Db        565 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 624

Qy        560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
                ||| | || |  |||||||    ||    |||||  |  | ||| |||| |||||||
Db        625 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 684

Qy        620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
                | |||  | |||||||||| |||||||  || |||||| | || || ||| |||| |
Db        685 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 744

Qy        680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
                ||||| | |||||||   |||| ||| | || ||||| ||||| |||||| | || ||||
Db        745 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 804

Qy        740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGAC 789
                |||| || ||  | || | | |   | | || |||||   |||   || |
Db        805 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAAGCCCCTGGAGCC 854
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RESULT 14
BX119589
LOCUS       BX119589                543 bp    mRNA    linear   EST 10-FEB-2003
DEFINITION  BX119589 Soares infant brain 1NIB Homo sapiens cDNA clone
            IMAGp998P20171 ; IMAGE:40608, mRNA sequence.
ACCESSION   BX119589
VERSION     BX119589.1  GI:28289997
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 543)
  AUTHORS   Ebert,L., Heil,O., Hennig,S., Neubert,P., Partsch,E., Peters,M.,
            Radelof,U., Schneider,D. and Korn,B.
  TITLE     Human UnigeneSet - RZPD3
  JOURNAL   Unpublished (2003)
COMMENT     Contact: Ina Rolfs
            RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
            Im Neuenheimer Feld 580, D-69120 Heidelberg, Germany
            RZPD; IMAGp998P20171.
            RZPDLIB; I.M.A.G.E. cDNA Clone Collection;
            Human UnigeneSet - RZPD3 (RZPDLIB No.972)
            http://www.rzpd.de/CloneCards/cgi-
            bin/showLib.pl.cgi/response?libNo=972 Contact: Ina Rolfs
```

RZPD Deutsches Ressourcenzentrum fuer Genomforschung GmbH
Heubnerweg 6, D-14059 Berlin, Germany
Tel: +49 30 32639 101
Fax: +49 30 32639 111
www.rzpd.de
This clone is available royalty-free from RZPD;
contact RZPD (clone@rzpd.de) for further information. Seq primer:
M13u, Primer sequence: CGTTGTAAAACGACGGCCAGT.

FEATURES Location/Qualifiers
source 1. .543
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGp998P20171 ; IMAGE:40608"
/sex="female"
/dev_stage="73 days post natal"
/lab_host="DH10B (ampicillin resistant)"
/clone_lib="Soares infant brain 1NIB"
/note="Organ: whole brain; Vector: Lafmid BA; Site_1: Not I; Site_2: Hind III; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' AACTGGAAGAATTCGCGGCCGCAGGAATTTTTTTTTTTTTTTTT 3']; double-stranded cDNA was ligated to Hind III adaptors (Pharmacia), digested with Not I and directionally cloned into the Not I and Hind III sites of the Lafmid BA vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

ORIGIN

Query Match 33.9%; Score 376.2; DB 13; Length 543;
Best Local Similarity 99.0%; Pred. No. 2.4e-66;
Matches 378; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        158 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 217

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        218 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 277

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        398 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 457

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              |||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db        458 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGNAAG 517
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Qy          361 GTCATCCCCTATCTACAGGCTG 382
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Db          518 GTCATCCCCTATCTACAGACAG 539


RESULT 15
CF147829
LOCUS       CF147829                 788 bp    mRNA    linear   EST 25-JUL-2003
DEFINITION  AGENCOURT_14740210 NIH_MGC_145 Homo sapiens cDNA clone
            IMAGE:6971890 5', mRNA sequence.
ACCESSION   CF147829
VERSION     CF147829.1  GI:33244097
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 788)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: GPCR Consortium
             cDNA Library Preparation: GPCR Consortium
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: IRBI02  row: a  column: 09
            High quality sequence start: 9
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FEATURES             Location/Qualifiers
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                     /clone="IMAGE:6971890"
                     /tissue_type="mixed"
                     /lab_host="DH10B"
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                     /note="Vector: pcDNA3.1; Site_1: varies by clone; Site_2:
                     varies by clone; ORFs were PCR-amplified and cloned into
                     pcDNA3.1 by the GPCR Consortium. Cloning sites vary by
                     clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
                     5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
                     For information about which gene each clones represents,
                     please visit our anonymous ftp site at
                     ftp://image.llnl.gov/image/rearrayed_plates/IRBI.preSV.dat
                     a Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             32.3%;  Score 359;  DB 14;  Length 788;
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Best Local Similarity 72.0%; Pred. No. 9.2e-63;
Matches 467; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

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Qy        80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
             | || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db       140 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 199

Qy       140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
             ||||||| ||||| |  ||  |    |||||||||||||| ||  | || |||   ||||
Db       200 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 259

Qy       200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
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             | || || |||||||| || || |||||    | |||||| || ||||  ||| | ||||
Db       320 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 379

Qy       320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
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Db       380 ATATCACCGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 439

Qy       380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
             | ||||| ||||| ||| | || || || || ||||  ||| || |||| || |||||||
Db       440 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 499

Qy       440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
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Db       500 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 559

Qy       500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
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Db       560 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 619

Qy       560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
              |||| | || | . |||||||    ||    |||||  |  | ||| |||| |||||||
Db       620 CTGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 679

Qy       620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
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Db       680 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 739

Qy       680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTG 728
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Search completed: October 15, 2004, 22:50:30
Job time : 3232.12 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 13:54:41 ; Search time 4497.38 Seconds
(without alignments)
10697.520 Million cell updates/sec

Title: US-10-070-532-3
Perfect score: 1110
Sequence: 1 atggagccctcagccacccc.....ttccctggagtctgctctaa 1110

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
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30: em_htg_hum:*
31: em_htg_inv:*
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33: em_htg_mus:*
34: em_htg_pln:*
35: em_htg_rod:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1110	100.0	1110	6	BD185453	BD185453 Human neu
2	1102	99.3	1110	6	AR216118	AR216118 Sequence
3	1079.4	97.2	1209	6	AR216117	AR216117 Sequence
4	1079.4	97.2	1564	6	E43974	E43974 Novel G pro
5	1079.4	97.2	1564	6	E50810	E50810 Novel G pro
6	1079.4	97.2	1564	6	E50811	E50811 Novel G pro
7	1079.4	97.2	1564	6	AX299473	AX299473 Sequence
8	1079.4	97.2	1564	6	AX299475	AX299475 Sequence
9	1079.4	97.2	1564	6	AX549082	AX549082 Sequence
10	1079.4	97.2	1564	6	AX746121	AX746121 Sequence
11	1079.4	97.2	1564	6	AX840912	AX840912 Sequence
12	1079.4	97.2	1564	9	AF041243	AF041243 Homo sapi
13	1078.4	97.2	1133	6	E43973	E43973 Novel G pro
14	1078.4	97.2	1133	6	AX746120	AX746120 Sequence
15	1078.4	97.2	1170	6	E43972	E43972 Novel G pro
16	1078.4	97.2	1170	6	AX746118	AX746118 Sequence
17	1077.8	97.1	1209	6	BD185452	BD185452 Human neu
18	1075.2	96.9	1116	6	AR216119	AR216119 Sequence
19	1075.2	96.9	1133	6	BD185454	BD185454 Human neu
20	1074.6	96.8	1278	6	AX280925	AX280925 Sequence
21	883.4	79.6	2200	10	AY336083	AY336083 Mus muscu
22	881	79.4	2469	10	AF041244	AF041244 Rattus no
23	688	62.0	843	6	AR109899	AR109899 Sequence
24	661	59.5	789	6	AR109632	AR109632 Sequence
25	661	59.5	789	6	E12154	E12154 cDNA encodi
26	661	59.5	789	6	AR300942	AR300942 Sequence
27	571.8	51.5	781	10	AF394596	AF394596 Mus muscu
28	545.6	49.2	3114	10	AF041246	AF041246 Rattus no
29	521.4	47.0	1545	10	AY336084	AY336084 Mus muscu
30	521.4	47.0	2117	10	AY336085	AY336085 Mus muscu
31	511.8	46.1	1633	6	E33974	E33974 cDNA clone
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35	507	45.7	1335	6	AX280927	AX280927 Sequence
36	505.4	45.5	1805	4	AF164626	AF164626 Canis fam
37	487.2	43.9	597	10	AY255599	AY255599 Mus muscu
38	322.8	29.1	382	4	AF499612	AF499612 Ovis arie
39	296.2	26.7	637	10	AF394597	AF394597 Mus muscu
40	275.2	24.8	328	4	AB092488	AB092488 Bos tauru
41	261.6	23.6	501	4	AF532967	AF532967 Ovis arie
42	241.2	21.7	344	9	F202078S03	AF202080 Homo sapi
43	241.2	21.7	9785	6	AR178605	AR178605 Sequence
44	241.2	21.7	9785	6	AX088174	AX088174 Sequence
45	241.2	21.7	9785	9	AY062030	AY062030 Homo sapi

ALIGNMENTS

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LOCUS       BD185453                1110 bp    DNA     linear   PAT 17-JUN-2003
DEFINITION  Human neuropeptide receptor.
ACCESSION   BD185453
VERSION     BD185453.1  GI:31877653
KEYWORDS    JP 2002360288-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1110)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.
  TITLE     Human neuropeptide receptor
  JOURNAL   Patent: JP 2002360288-A 2 17-DEC-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Unidentified
            PN   JP 2002360288-A/2
            PD   17-DEC-2002
            PF   02-MAY-2002 JP 2002130838
            PI   DANIEL R SOPPET,YI LI,CRAIG A ROSEN
            PC   C12N15/09,A61K31/7088,A61K38/00,A61K45/00,A61K48/00,A61P3/04,
            PC   A61P3/06,
            PC   A61P3/10,A61P9/10,A61P9/12,A61P25/08,A61P25/18,A61P25/22, PC
           A61P25/28,
            PC   A61P35/00,A61P43/00,C07K14/705,C07K16/24,C12N1/15,C12N1/19, PC
              C12N1/21,
            PC   C12N5/10,C12Q1/68,C12N15/00,C12N5/00,A61K37/02 CC
            Strandedness: Single;
            CC   Topology: Linear;
            CC   Human neuropeptide receptor
            FH   Key             Location/Qualifiers
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            FT                   /organism='Unidentified'.
FEATURES             Location/Qualifiers
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ORIGIN
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Query Match 100.0%; Score 1110; DB 6; Length 1110;
Best Local Similarity 100.0%; Pred. No. 2.6e-210;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

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Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

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Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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Db       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110


RESULT 2
AR216118
LOCUS       AR216118                1110 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 3 from patent US 6410701.
ACCESSION   AR216118
VERSION     AR216118.1  GI:23314431
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1110)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.
  TITLE     Human neuropeptide receptor
  JOURNAL   Patent: US 6410701-A 3 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .1110
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ORIGIN

  Query Match             99.3%;  Score 1102;  DB 6;  Length 1110;
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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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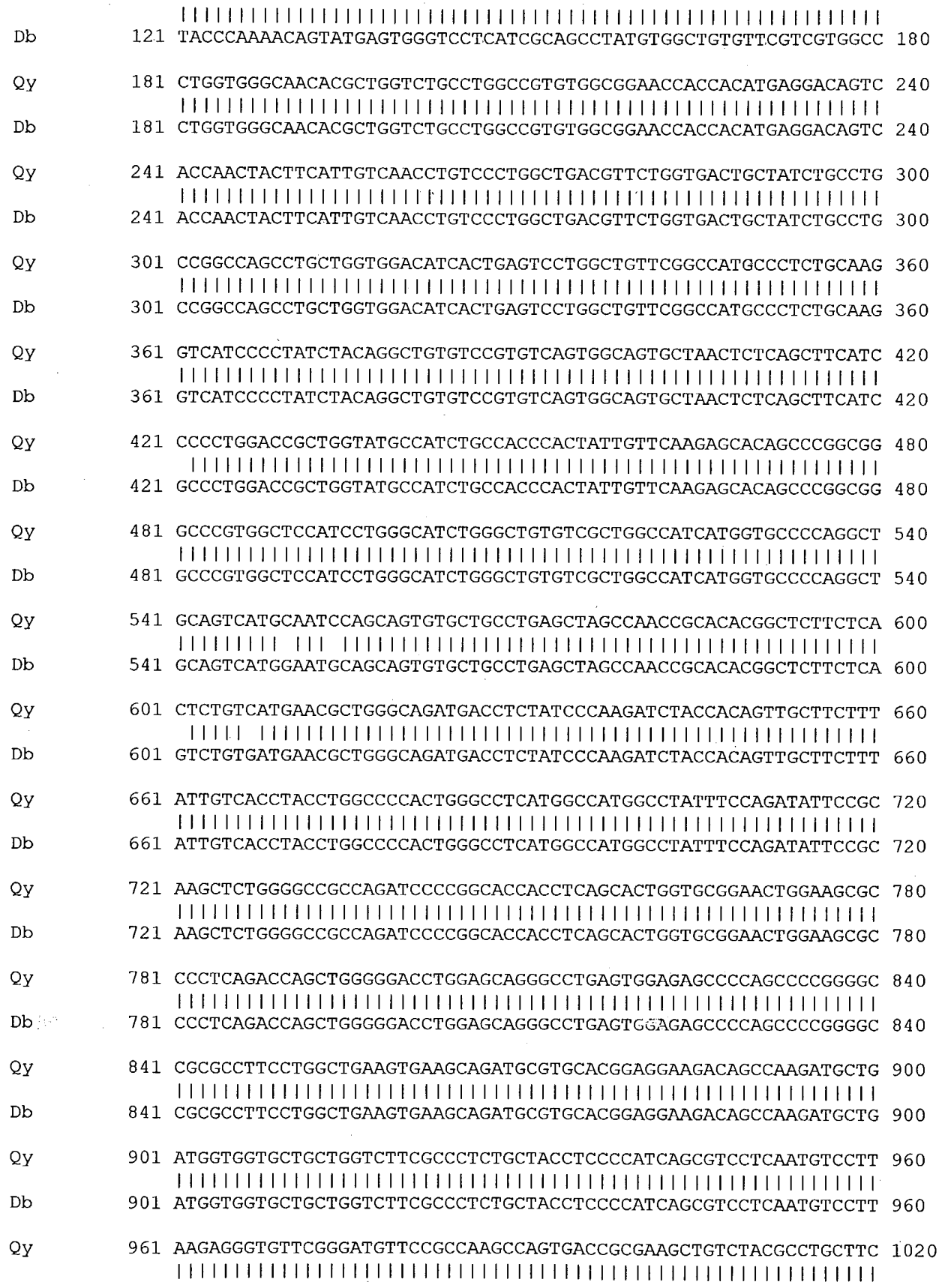

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Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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Db       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110


RESULT 3
AR216117
LOCUS       AR216117                1209 bp    DNA     linear   PAT 25-SEP-2002
DEFINITION  Sequence 1 from patent US 6410701.
ACCESSION   AR216117
VERSION     AR216117.1  GI:23314430
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1209)
  AUTHORS   Soppet,D.R., Li,Y. and Rosen,C.A.
  TITLE     Human neuropeptide receptor
  JOURNAL   Patent: US 6410701-A 1 25-JUN-2002;
FEATURES             Location/Qualifiers
     source          1. .1209
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ORIGIN

  Query Match             97.2%;  Score 1079.4;  DB 6;  Length 1209;
  Best Local Similarity   99.4%;  Pred. No. 3.1e-204;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

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Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

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Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGC 1089
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Db       1081 CTCAGTGGC 1089
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RESULT 4
E43974

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LOCUS       E43974                  1564 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION   E43974
VERSION     E43974.1  GI:18625173
KEYWORDS    JP 2000106888-A/3.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL   Patent: JP 2000106888-A 3 18-APR-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000106888-A/3
            PD   18-APR-2000
            PF   21-JUL-1999 JP 1999206116
            PR   30-APR-1997 US    08/846705
            PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
            PC   C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
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            FH   Key             Location/Qualifiers
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  Query Match             97.2%;  Score 1079.4;  DB 6;  Length 1564;
  Best Local Similarity   99.4%;  Pred. No. 3e-204;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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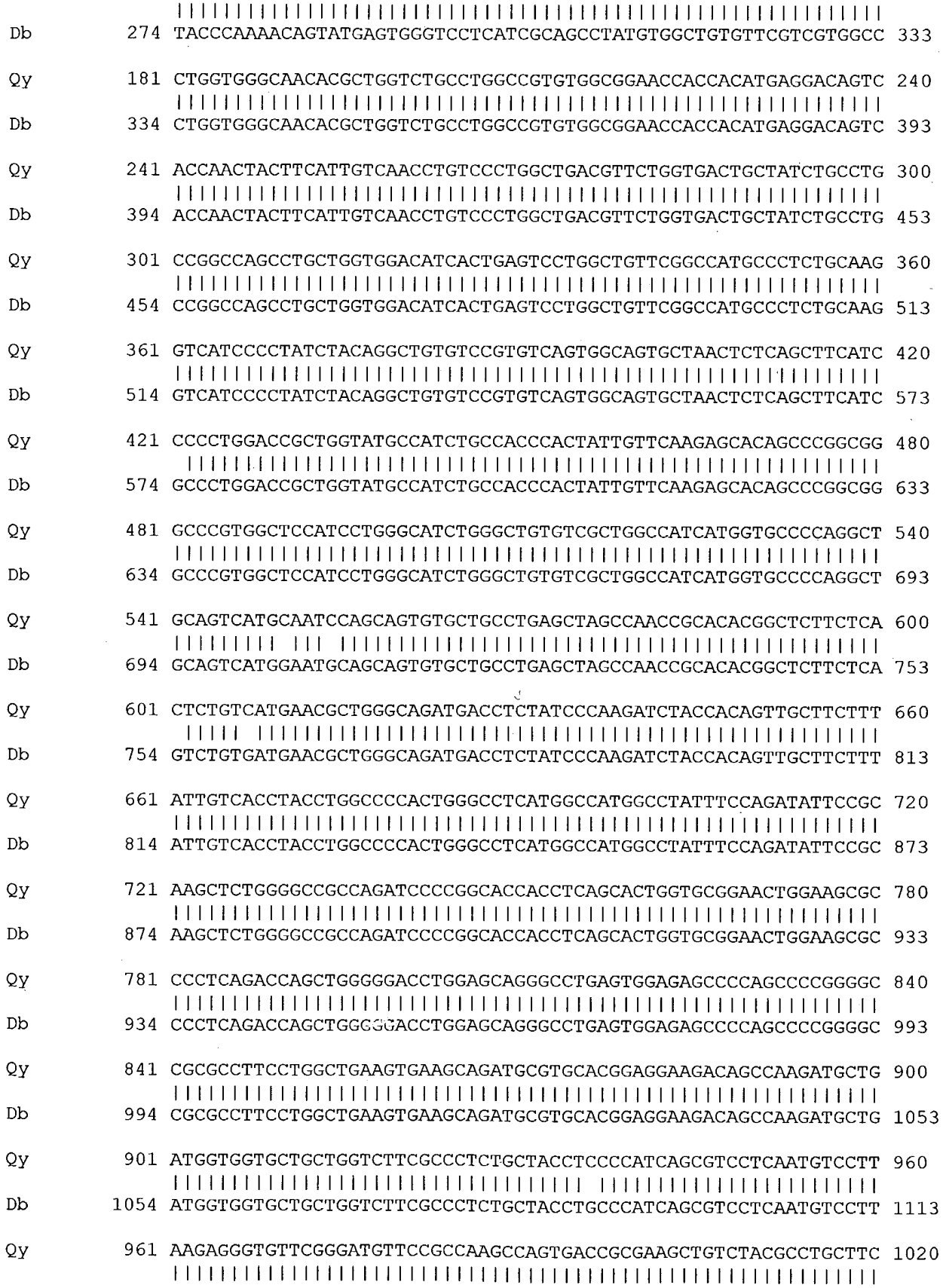
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Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy 421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813
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Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
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Db       1234 CTCAGTGGC 1242


RESULT 5
E50810
LOCUS       E50810                  1564 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Novel G protein-bound receptor (HFGAN 72X).
ACCESSION   E50810
VERSION     E50810.1  GI:13023197
KEYWORDS    JP 2000060578-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Derk,J.B. and Catharine,E.E.
  TITLE     Novel G protein-bound receptor (HFGAN 72X)
  JOURNAL   Patent: JP 2000060578-A 1 29-FEB-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000060578-A/1
            PD   29-FEB-2000
            PF   21-JUL-1999 JP 1999206115
            PR   30-APR-1997 US    08/846704
            PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
            PC   C12N15/09,A61K31/70,A61K38/00,A61K39/00,A61K39/395,A61K39/395,
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FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             97.2%;  Score 1079.4;  DB 6;  Length 1564;
  Best Local Similarity   99.4%;  Pred. No. 3e-204;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

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Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

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Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

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Qy       1081 CTCAGTGGC 1089
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RESULT 6
E50811
LOCUS       E50811                  1564 bp    DNA     linear   PAT 18-JUN-2001
DEFINITION  Novel G protein-bound receptor (HFGAN 72X).
ACCESSION   E50811
VERSION     E50811.1  GI:13023198
KEYWORDS    JP 2000060578-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Derk,J.B. and Catharine,E.E.
  TITLE     Novel G protein-bound receptor (HFGAN 72X)
  JOURNAL   Patent: JP 2000060578-A 2 29-FEB-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000060578-A/2
            PD   29-FEB-2000
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            PR   30-APR-1997 US    08/846704
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FEATURES             Location/Qualifiers
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ORIGIN

Query Match 97.2%; Score 1079.4; DB 6; Length 1564;
Best Local Similarity 99.4%; Pred. No. 3e-204;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

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Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy       1081 CTCAGTGGC 1089
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DEFINITION  Sequence 1 from Patent EP1154019.
ACCESSION   AX299473
VERSION     AX299473.1  GI:17129230
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (hfgan72x)
  JOURNAL   Patent: EP 1154019-A 1 14-NOV-2001;
            SmithKline Beecham Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             97.2%;  Score 1079.4;  DB 6;  Length 1564;
  Best Local Similarity   99.4%;  Pred. No. 3e-204;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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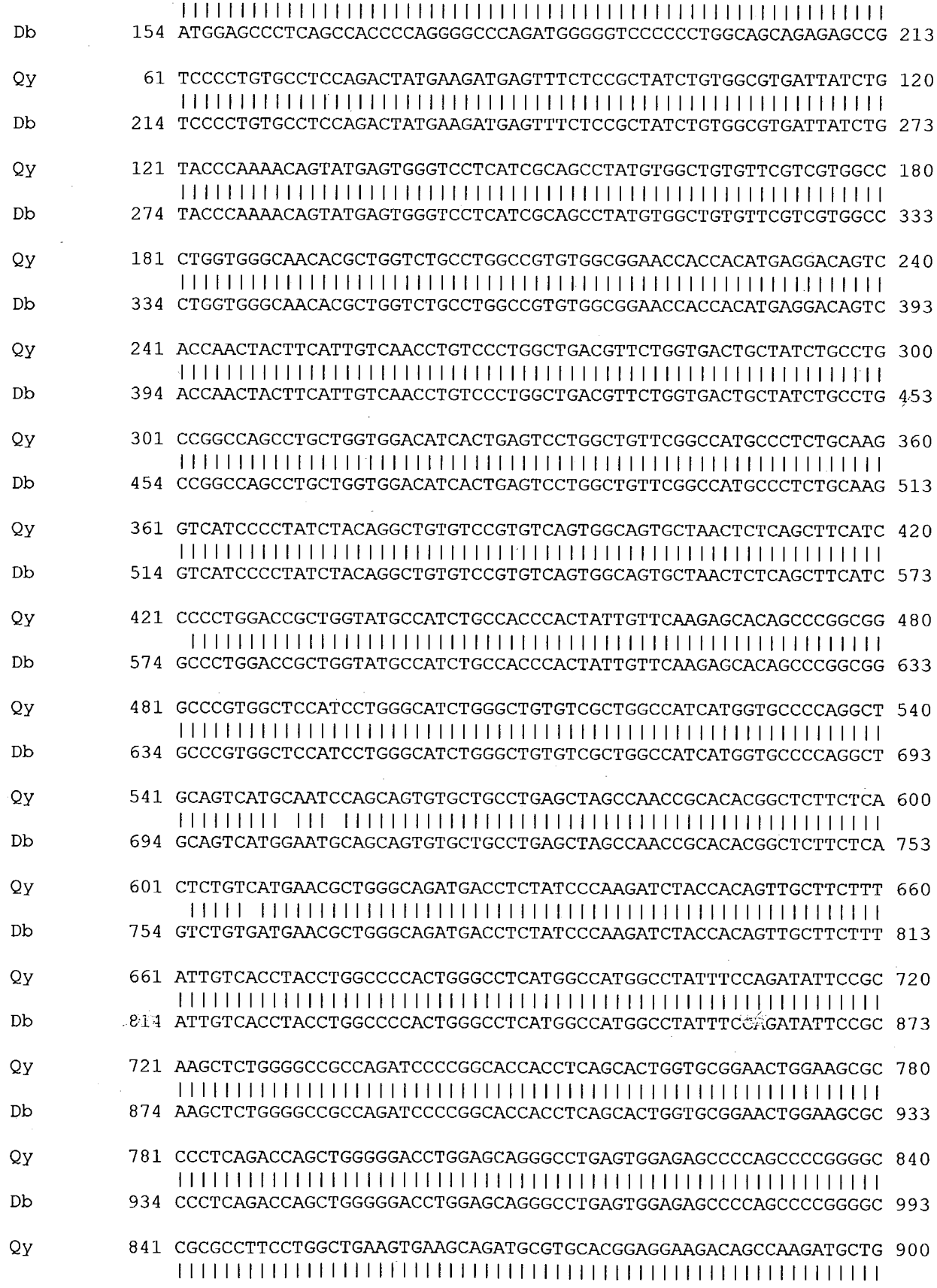
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Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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RESULT 8
AX299475
LOCUS       AX299475                1564 bp    DNA     linear   PAT 26-NOV-2001
DEFINITION  Sequence 3 from Patent EP1154019.
ACCESSION   AX299475
VERSION     AX299475.1  GI:17129231
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (hfgan72x)
  JOURNAL   Patent: EP 1154019-A 3 14-NOV-2001;
            SmithKline Beecham Corporation (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             97.2%;  Score 1079.4;  DB 6;  Length 1564;
  Best Local Similarity   99.4%;  Pred. No. 3e-204;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Qy       1081 CTCAGTGGC 1089
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RESULT 9
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LOCUS       AX549082               1564 bp    DNA     linear   PAT 26-NOV-2002
DEFINITION  Sequence 367 from Patent WO02061087.
ACCESSION   AX549082
VERSION     AX549082.1  GI:25813851
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
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            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Burmer,G.C., Roush,C.L. and Brown,J.P.
  TITLE     Antigenic peptides, such as for G protein-coupled receptors
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  JOURNAL   Patent: WO 02061087-A 367 08-AUG-2002;
            Lifespan Biosciences, Inc. (US)
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             97.2%;  Score 1079.4;  DB 6;  Length 1564;
  Best Local Similarity   99.4%;  Pred. No. 3e-204;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

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Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy      1081 CTCAGTGGC 1089
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Db      1234 CTCAGTGGC 1242
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RESULT 10
AX746121
LOCUS AX746121 1564 bp DNA linear PAT 12-JUN-2003
DEFINITION Sequence 4 from Patent EP1156110.
ACCESSION AX746121
VERSION AX746121.1 GI:31744927
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bergsma,D.J. and Ellis,C.E.
TITLE G-protein coupled receptor (HFGAN72Y)
JOURNAL Patent: EP 1156110-A 4 21-NOV-2001;
SMITHKLINE BEECHAM CORPORATION (US)
FEATURES Location/Qualifiers
source 1. .1564
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/note="HGS EST 554692"
ORIGIN

Query Match 97.2%; Score 1079.4; DB 6; Length 1564;
Best Local Similarity 99.4%; Pred. No. 3e-204;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db        934 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
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Db       1234 CTCAGTGGC 1242
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RESULT 11
AX840912
LOCUS AX840912 1564 bp DNA linear PAT 16-DEC-2003
DEFINITION Sequence 8 from Patent WO03075945.
ACCESSION AX840912
VERSION AX840912.1 GI:39979051
KEYWORDS .
SOURCE Homo sapiens (human)

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  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Eulenberg,K., Steuernagel,A., Haeder,T. and Broenner,G.
  TITLE     Cg8327, cg10823, cg18418, cg15862, cg3768, cg11447 and cg16750
            homologous proteins involved in the regulation of energy
            homeostasis
  JOURNAL   Patent: WO 03075945-A 8 18-SEP-2003;
            DeveloGen Aktiengesellschaft fuer entwicklungsbiologische;
            Forschung (DE)
FEATURES             Location/Qualifiers
     source          1. .1564
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ORIGIN

  Query Match             97.2%;  Score 1079.4;  DB 6;  Length 1564;
  Best Local Similarity   99.4%;  Pred. No. 3e-204;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
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Db       1234 CTCAGTGGC 1242
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RESULT 12
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LOCUS       AF041243               1564 bp    mRNA    linear   PRI 24-FEB-1998
DEFINITION  Homo sapiens orexin receptor-1 mRNA, complete cds.
ACCESSION   AF041243
VERSION     AF041243.1  GI:2897123
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1564)
  AUTHORS   Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M.,
            Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P.,
            Wilson,S., Arch,J.R.S., Buckingham,R.E., Haynes,A.C., A. Carr,S.A.,
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Annan,R.S., McNulty,D.E., Liu,W.-S., Terrett,J.A.,
Elshourbagy,N.A., Bergsma,D.J. and Yanagisawa,M.
TITLE Orexins and orexin receptors: a family of hypothalamic neuropeptides and G protein-coupled receptors that regulate feeding behavior
JOURNAL Cell 92 (4), 573-585 (1998)
MEDLINE 98150861
PUBMED 9491897
REFERENCE 2 (bases 1 to 1564)
AUTHORS Sakurai,T., Amemiya,A., Ishii,M., Matsuzaki,I., Chemelli,R.M., Tanaka,H., Williams,S.C., Richardson,J.A., Kozlowski,G.P., Wilson,S., Arch,J.R.S., Buckingham,R.E., Haynes,A.C., A. Carr,S.A., Annan,R.S., McNulty,D.E., Liu,W.-S., Terrett,J.A., Elshourbagy,N.A., Bergsma,D.J. and Yanagisawa,M.
TITLE Direct Submission
JOURNAL Submitted (07-JAN-1998) HHMI/Department of Molecular Genetics, University of Texas Southwestern Medical Center at Dallas, 5323 Harry Hines Blvd., Rm. Y5.224, Dallas, TX 75235-9050, USA
FEATURES Location/Qualifiers
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AVYACFTFSHWLVYANSAANPIIYNFLSGKFREQFKAAFSCCLPGLGPCGSLKAPSPR
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ORIGIN

Query Match 97.2%; Score 1079.4; DB 9; Length 1564;
Best Local Similarity 99.4%; Pred. No. 3e-204;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db       694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy       601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db       754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db       874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy       781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db      1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy       1081 CTCAGTGGC 1089
                ||||||||
Db       1234 CTCAGTGGC 1242


RESULT 13
E43973
LOCUS       E43973                  1133 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION   E43973
VERSION     E43973.1  GI:18625172
KEYWORDS    JP 2000106888-A/2.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1133)
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL   Patent: JP 2000106888-A 2 18-APR-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000106888-A/2
            PD   18-APR-2000
            PF   21-JUL-1999 JP 1999206116
            PR   30-APR-1997 US    08/846705
            PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
            PC   C12N15/09,A61K38/00,A61K38/00,A61K45/00,A61K48/00,A61P1/00, PC
              A61P1/14,
            PC   A61P9/02,A61P9/04,A61P9/10,A61P9/12,A61P11/06,A61P13/02, PC
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            PC   A61P43/00,
            PC   C07K14/705,C07K16/28,C12N1/21,C12N5/10,C12P21/02,G01N33/566,
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            PC   C12P21/08,(C12N15/09,C12R1:91),(C12P21/02,C12R1:91),C12N15/00,
            PC   A61K37/02,
            PC   A61K37/02,C12N5/00,(C12N15/00,C12R1:91)
            CC   Strandedness: Single;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers
            FT   source          1. .1133
            FT                   /organism='Unidentified'.
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ORIGIN

  Query Match             97.2%;  Score 1078.4;  DB 6;  Length 1133;
  Best Local Similarity   99.4%;  Pred. No. 4.9e-204;
  Matches 1082;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;
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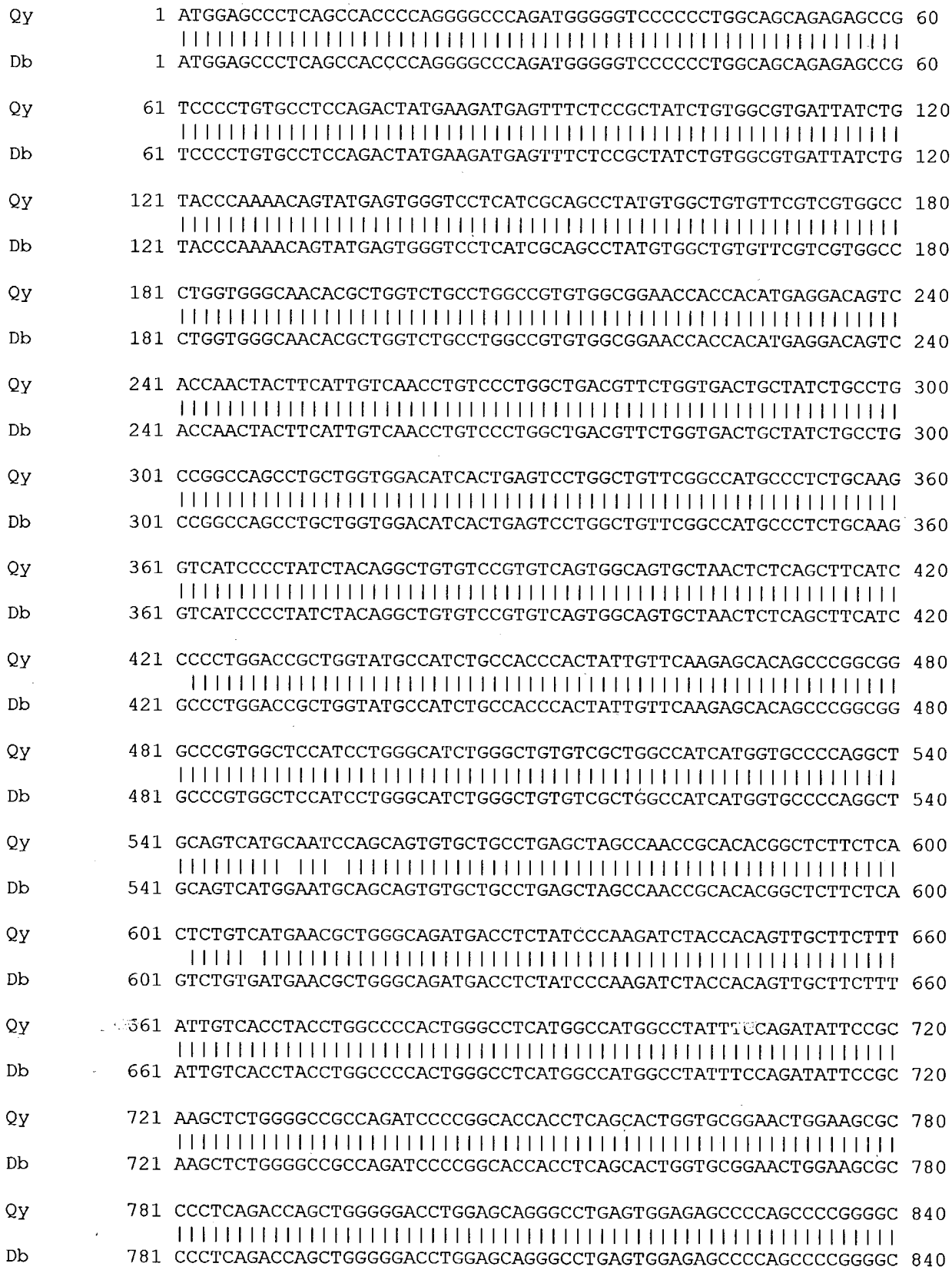

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Qy       1081 CTCAGTGG 1088
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Db       1081 CTCAGTGG 1088


RESULT 14
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DEFINITION  Sequence 3 from Patent EP1156110.
ACCESSION   AX746120
VERSION     AX746120.1  GI:31744926
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     G-protein coupled receptor (HFGAN72Y)
  JOURNAL   Patent: EP 1156110-A 3 21-NOV-2001;
            SMITHKLINE BEECHAM CORPORATION (US)
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ORIGIN

  Query Match             97.2%;  Score 1078.4;  DB 6;  Length 1133;
  Best Local Similarity   99.4%;  Pred. No. 4.9e-204;
  Matches 1082;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Qy       1081 CTCAGTGG 1088
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LOCUS       E43972                  1170 bp    DNA     linear   PAT 31-JAN-2002
DEFINITION  Novel G protein-coupled receptor (HFGAN72Y).
ACCESSION   E43972
VERSION     E43972.1  GI:18625171
KEYWORDS    JP 2000106888-A/1.
SOURCE      unidentified
  ORGANISM  unidentified
            unclassified.
REFERENCE   1  (bases 1 to 1170)
  AUTHORS   Bergsma,D.J. and Ellis,C.E.
  TITLE     Novel G protein-coupled receptor (HFGAN72Y)
  JOURNAL   Patent: JP 2000106888-A 1 18-APR-2000;
            SMITHKLINE BEECHAM CORP
COMMENT     OS   Unidentified
            PN   JP 2000106888-A/1
            PD   18-APR-2000
            PF   21-JUL-1999 JP 1999206116
            PR   30-APR-1997 US    08/846705
            PI   DERK J BERGSMA,CATHARINE ELIZABETH ELLIS
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Query Match 97.2%; Score 1078.4; DB 6; Length 1170;
Best Local Similarity 99.4%; Pred. No. 4.9e-204;
Matches 1082; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Title: US-10-070-532-3
Perfect score: 1110
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1079.4	97.2	1209	2	AAT42826	Aat42826 Neuropept
4	1079.4	97.2	1564	2	AAV63468	Aav63468 cDNA enco
5	1079.4	97.2	1564	2	AAV68514	Aav68514 Nucleotid
6	1079.4	97.2	1564	4	AAF32103	Aaf32103 Human HFG
7	1079.4	97.2	1564	6	ABA96021	Aba96021 HGS EST 5

8	1079.4	97.2	1564	6	AAI64173	Aai64173 HFGAN72X
9	1079.4	97.2	1564	6	AAI64172	Aai64172 Human HFG
10	1079.4	97.2	1564	7	ABZ42789	Abz42789 Human ore
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18	1075.2	96.9	1133	2	AAT42828	Aat42828 Neuropept
19	1074.6	96.8	1278	5	ABI98014	Abi98014 Non-endog
20	1031.4	92.9	1278	4	AAD09335	Aad09335 Cynomolgo
21	905	81.5	1281	5	AAC85974	Aac85974 Dog orexi
22	661	59.5	789	2	AAT13909	Aat13909 Rabbit G-
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25	511.8	46.1	1843	7	ABZ42790	Abz42790 Human ore
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ALIGNMENTS

RESULT 1
AAS00492
ID AAS00492 standard; cDNA; 1110 BP.
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AC AAS00492;
XX
DT 17-MAY-2001 (first entry)
XX
DE Human neuropeptide receptor splice variant 1 cDNA.
XX
KW Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
KW nervous system disorder; hyperproliferative disorder; diabetes mellitus;
KW cardiovascular disorder; autoimmune disorder; infectious disorder;
KW eating behaviour disorder; narcolepsy; neurological disease;

KW narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;
KW protein co-ordinate data; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1110
FT /*tag= a
FT /product= "neuropeptide receptor splice variant 1"
XX
PN WO200117532-A1.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024518.
XX
PR 10-SEP-1999; 99US-00393696.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 2001-183276/18.
DR P-PSDB; AAU00439.
XX
PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,
PT useful for preventing, treating or ameliorating obesity, narcolepsy,
PT neurological disease and addiction to narcotics, nicotine and alcohol.
XX
PS Claim 4; Fig 2; 385pp; English.
XX
CC The present sequence encodes for human neuropeptide receptor splice
CC variant 1. Two splice variants (AAU00439-AAU00440) and a possible mutant
CC (AAU00442) of a novel human neuropeptide receptor (AAU00438) are
CC described. The neuropeptide receptor shows sequence homology to the
CC neuropeptide Y receptor. Polypeptides and polynucleotides of the
CC neuropeptide receptor are useful for diagnosing, preventing, or treating
CC a pathological condition in a subject related to the central nervous and
CC peripheral nervous systems (CNS and PNS). The polypeptides and
CC polynucleotides may be used to treat hyperproliferative, cardiovascular,
CC autoimmune, nervous system or infectious disorders e.g. cancer, heart
CC disease, rheumatoid arthritis, Alzheimer's disease, HIV infection and
CC diabetes mellitus. In particular they are useful for preventing, treating
CC or ameliorating a medical condition in a mammal such as obesity/eating
CC behaviour disorders, narcolepsy, neurological disease, addiction to
CC narcotics, nicotine and alcohol, chronic pain, acute pain, migraine
CC headaches and anxiety disorders. The polynucleotides encoding the
CC neuropeptide receptor can also be used in gene therapy methods for
CC treating such diseases
XX
SQ Sequence 1110 BP; 194 A; 369 C; 300 G; 247 T; 0 U; 0 Other;

Query Match 100.0%; Score 1110; DB 4; Length 1110;
Best Local Similarity 100.0%; Pred. No. 4.6e-253;
Matches 1110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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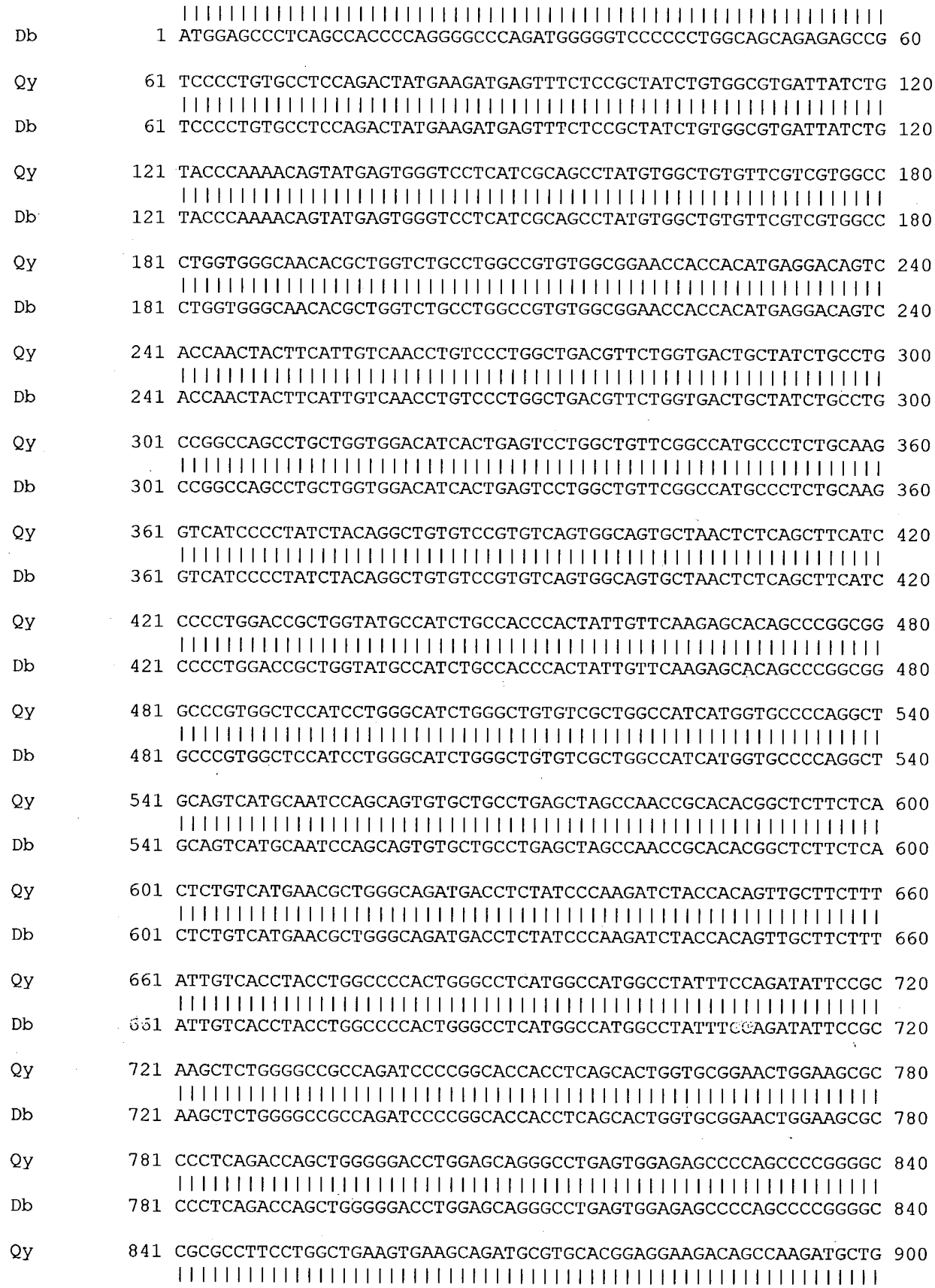
Db 1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
Db 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
Qy 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
Db 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
Db 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
Db 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
Db 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Qy 421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
Db 421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
Db 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
Qy 541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
Db 541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
Qy 601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
Db 601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
Db 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
Db 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
Db 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

```
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
              |||||||||||||||||||||||||||||
Db       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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RESULT 2
AAT42827
ID AAT42827 standard; cDNA; 1110 BP.
XX
AC AAT42827;
XX
DT 22-FEB-1997 (first entry)
XX
DE Neuropeptide receptor splice variant-1 gene.
XX
KW Human; neuropeptide receptor; splice variant; drug screening;
KW receptor-agonist; receptor-antagonist; anorectic; antitumour;
KW anticholesterolemic; neuroprotective; anticonvulsant; hypotensive;
KW sedative; diagnostic; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO9634877-A1.
XX
PD 07-NOV-1996.
XX
PF 05-MAY-1995; 95WO-US005616.
XX
PR 05-MAY-1995; 95WO-US005616.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 1996-506094/50.
DR P-PSDB; AAW06125.
XX
PT Human neuro-peptide receptor polypeptide(s) - used to identify
PT antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT obesity, Alzheimer's disease, epilepsy, etc.
XX
PS Disclosure; Page 50-51; 77pp; English.
XX

CC The sequence encodes human neuropeptide receptor splice variant-1, which
CC retains activity corresponding to the mature receptor (encoded by
CC AAT42826). The receptor gene has been isolated from from a human adult
CC hypothalamus cDNA library, and is structurally related to the G-protein-
CC coupled receptor family. The receptor may be used in a drug screening
CC assay for isolation of receptor-agonists and -antagonists, which may be
CC used as anorectic, antitumour, anticholesterolemic, neuroprotective,
CC anticonvulsant, hypotensive or sedative drugs, etc. The DNA may also be
CC used in genetic disease diagnosis or gene therapy. The receptor and its
CC corresponding antibody may also be used in therapy and diagnosis
XX
SQ Sequence 1110 BP; 194 A; 364 C; 305 G; 247 T; 0 U; 0 Other;

Query Match 99.3%; Score 1102; DB 2; Length 1110;
Best Local Similarity 99.5%; Pred. No. 3.6e-251;
Matches 1105; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
              |||||||||||||||||||||||||||||
Db       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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RESULT 3
AAT42826
ID   AAT42826 standard; cDNA; 1209 BP.
XX
AC   AAT42826;
XX
DT   22-FEB-1997  (first entry)
XX
DE   Neuropeptide receptor gene.
XX
KW   Human; neuropeptide receptor; drug screening; receptor-agonist;
KW   receptor-antagonist; anorectic; antitumour; anticholesterolemic;
KW   neuroprotective; anticonvulsant; hypotensive; sedative; diagnostic;
KW   gene therapy; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   primer_bind     complement(1. .18)
FT                   /*tag=  a
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FT                      /note= "Binds primer AAT42829"
FT   misc_difference    151. .153
FT                      /*tag=  b
FT                      /codon= seq:CCA, aa:Ala
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FT                      /note= "Binds primers AAT42830 and AAT42832"
XX
PN   WO9634877-A1.
XX
PD   07-NOV-1996.
XX
PF   05-MAY-1995;   95WO-US005616.
XX
PR   05-MAY-1995;   95WO-US005616.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Soppet DR,  Li Y,  Rosen CA;
XX
DR   WPI; 1996-506094/50.
DR   P-PSDB; AAW06124.
XX
PT   Human neuro-peptide receptor polypeptide(s) - used to identify
PT   antagonists and agonists to such polypeptide(s), e.g. in the treatment of
PT   obesity, Alzheimer's disease, epilepsy, etc.
XX
PS   Claim 6; Page 48-49; 77pp; English.
XX
CC   The sequence encodes a human neuropeptide receptor, and has been mapped
CC   to human chromosome 1q31-34. The sequence has been isolated from a human
CC   adult hypothalamus cDNA library, and is structurally related to the G-
CC   protein-coupled receptor family. Splice variants are given in AAT42827-
CC   28. The sequence may be amplified by PCR with e.g. primers AAT42829-34
CC   for expression in a host cell. The recombinant receptor may be used in a
CC   drug screening assay for isolation of receptor-agonists and -antagonists,
CC   which may be used as anorectic, antitumour, anticholesterolemic,
CC   neuroprotective, anticonvulsant, hypotensive or sedative drugs, etc. The
CC   DNA may also be used in genetic disease diagnosis or gene therapy. The
CC   receptor and its corresponding antibody may also be used in therapy and
CC   diagnosis
XX
SQ   Sequence 1209 BP; 206 A; 402 C; 330 G; 271 T; 0 U; 0 Other;

  Query Match             97.2%;  Score 1079.4;  DB 2;  Length 1209;
  Best Local Similarity   99.4%;  Pred. No. 8.3e-246;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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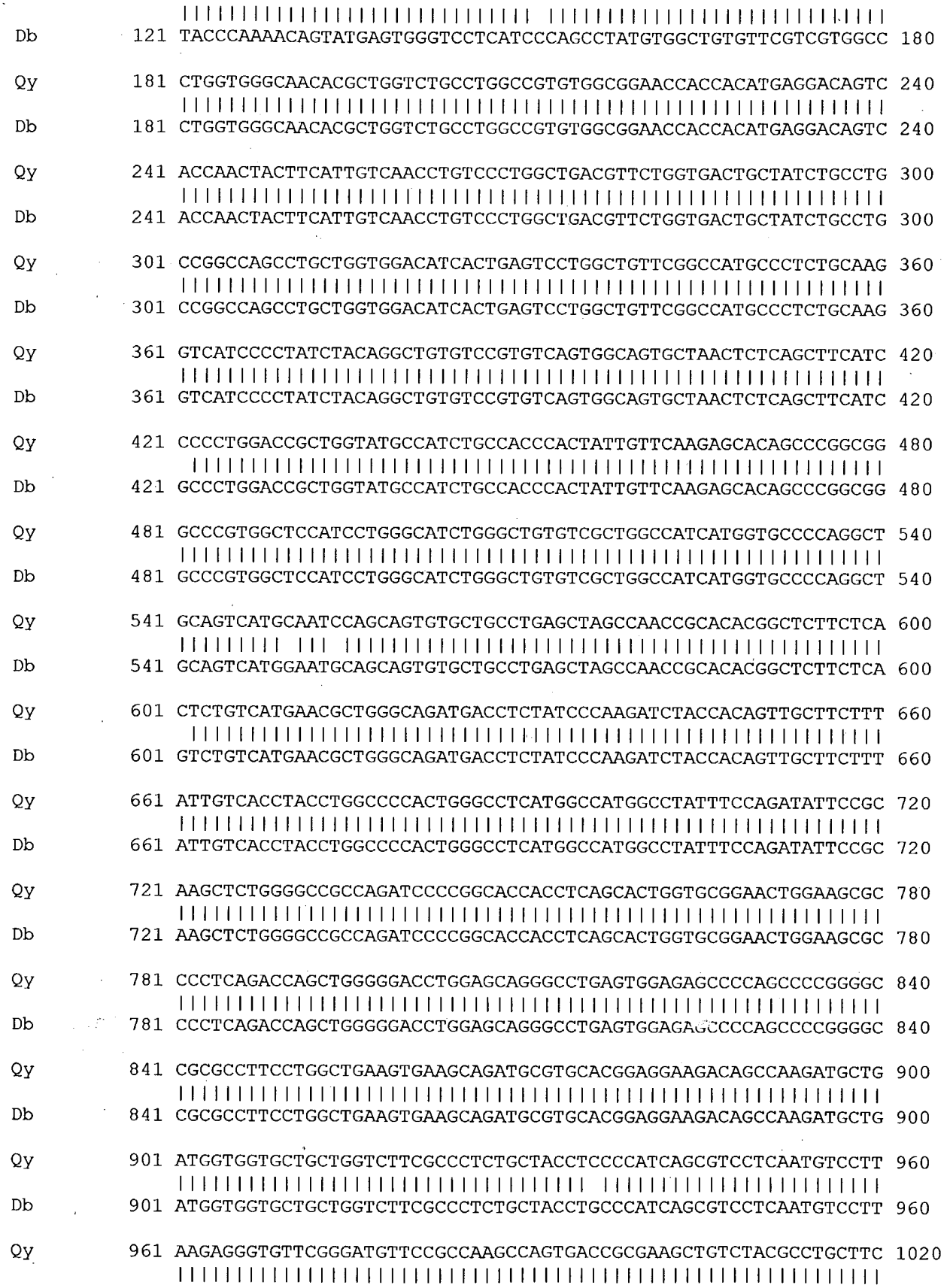

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Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1081 CTCAGTGGC 1089
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RESULT 4
AAV63468
ID AAV63468 standard; cDNA; 1564 BP.
XX
AC AAV63468;
XX
DT 26-JAN-1999 (first entry)
XX
DE cDNA encoding G-protein coupled receptor (HFGAN72X) polypeptide.
XX
KW G-protein coupled receptor; HFGAN72X; HIV infection; anorexia; cancer;
KW bulimia; asthma; Parkinson's disease; acute heart failure;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW benign prostatic hypertrophy; neurological disorder; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   154. .1431
FT   /*tag= a
FT   /product= "HFGAN72X"
XX
PN EP875566-A2.
XX
PD 04-NOV-1998.
XX
PF 27-OCT-1997; 97EP-00308563.
XX
PR 30-APR-1997; 97US-00846704.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 1998-599432/48.
DR P-PSDB; AAW80456.
XX
PT New human G-protein coupled receptor HFGAN72X polypeptide and
PT polynucleotide - useful as diagnostic reagents and for treating e.g. HIV
PT infection, cancer and Parkinson's disease.
XX
PS Claim 3; Page 7; 24pp; English.
XX
CC The present sequence encodes a G-protein coupled receptor (HFGAN72X)
CC polypeptide. HFGAN72X polypeptides and polynucleotides are useful for
CC diagnosing diseases related to over or under expression of HFGAN72X

CC proteins by identifying mutations in the HFGAN72X gene using HFGAN72X
CC probes, or determining HFGAN72X protein or mRNA expression levels.
CC HFGAN72X polypeptides are also useful for screening for compounds which
CC affect activity of the protein. Diseases that can be treated with
CC HFGAN72X include HIV infections, pain, anorexia, cancers, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, ulcers, allergies, benign prostatic hypertrophy,
CC and psychotic and neurological disorders
XX
SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 97.2%; Score 1079.4; DB 2; Length 1564;
Best Local Similarity 99.4%; Pred. No. 8.9e-246;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db         754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy         661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy         721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy         781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy         841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy         901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
               |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy         961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy        1021 ACCTTCTCCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1174 ACCTTCTCCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy        1081 CTCAGTGGC 1089
               |||||||||
Db        1234 CTCAGTGGC 1242
```

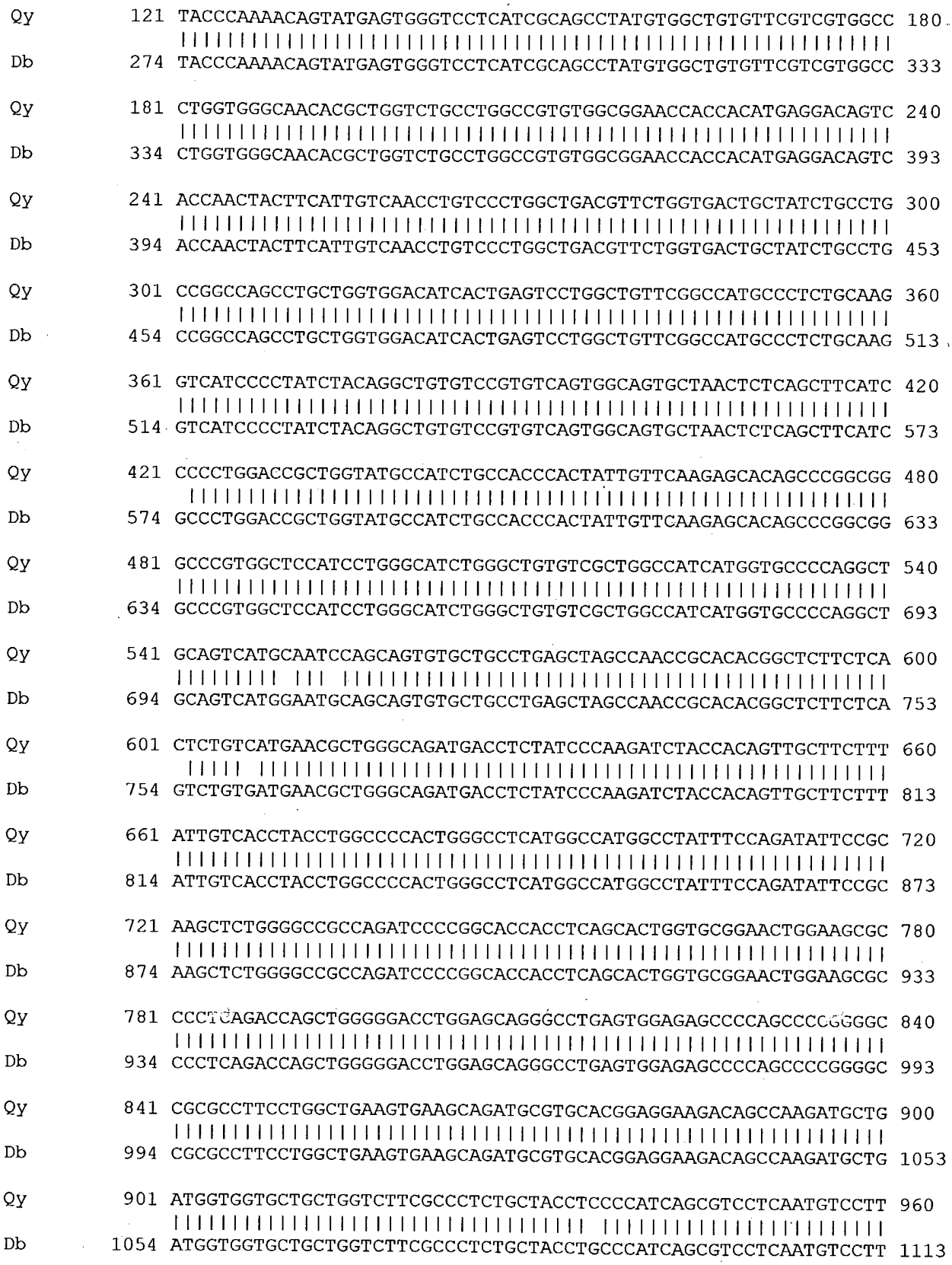
RESULT 5
AAV68514
ID AAV68514 standard; cDNA; 1564 BP.
XX
AC AAV68514;
XX
DT 29-JAN-1999 (first entry)
XX
DE Nucleotide sequence of a probe HGS EST 554692.
XX
KW Probe HGS EST 554692; G-protein coupled receptor family; HFGAN72Y;
KW mutation; probe; agonist; antagonist; activation; inhibition;
KW gene therapy; antibody; immune response; vaccine; HIV-1; HIV-2; cancer;
KW anorexia; bulimia; asthma; Parkinson's disease; acute heart failure;
KW hypotension; hypertension; urinary retention; osteoporosis;
KW angina pectoris; myocardial infarction; ulcer; allergies;
KW psychotic disorder; neurological disorder; gene mapping; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX

PN EP875565-A2.
XX
PD 04-NOV-1998.
XX
PF 27-OCT-1997; 97EP-00308554.
XX
PR 30-APR-1997; 97US-00846705.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis C;
XX
DR WPI; 1998-570286/49.
XX
PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of HIV
PT infections, cancer, osteoporosis and Parkinson's disease.
XX
PS Example 1; Page 19-20; 22pp; English.
XX
CC This is the nucleotide sequence of the probe HGS EST 554692 used in the
CC method of the invention involving the G-protein coupled receptor,
CC HFGAN72Y. Its polypeptides and polynucleotides are useful for diagnosing
CC susceptibility to diseases by detecting mutations in the HFGAN72Y gene
CC using probes containing the HFGAN72Y nucleotide sequence, and can
CC diagnose diseases associated with HFGAN72Y imbalance by determining
CC HFGAN72Y polypeptide or mRNA expression levels. Agonists/antagonists can
CC be used in treatment to activate/inhibit HFGAN72Y activity, in addition
CC to direct administration of antisense sequences to prevent expression, or
CC HFGAN72Y polypeptides to treat conditions associated with a lack HFGAN72Y
CC protein. Gene therapy may also be used to affect endogenous HFGAN72Y
CC polypeptide production. HFGAN72Y antibodies are useful for inducing an
CC immune response to immunise and prevent diseases, and for isolating
CC HFGAN72Y clones or purifying the polypeptides by affinity chromatography.
CC HFGAN72Y polypeptides can be administered directly or as a vaccine to
CC inoculate against diseases. Diseases diagnosed, prevented or treated
CC include HIV-1 or HIV-2 infections, pain, cancers, anorexia, bulimia,
CC asthma, Parkinson's disease, acute heart failure, hypotension,
CC hypertension, urinary retention, osteoporosis, angina pectoris,
CC myocardial infarction, ulcers; allergies, benign prostatic hypertrophy,
CC and psychotic and neurological disorders. The HFGAN72Y polypeptide is
CC also useful for mapping the gene to a chromosome, allowing gene
CC inheritance to be studied through linkage analysis
XX
SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 97.2%; Score 1079.4; DB 2; Length 1564;
Best Local Similarity 99.4%; Pred. No. 8.9e-246;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273
```


Qy 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
Db 274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333
Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
Db 334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393
Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453
Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
Db 454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513
Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573
Qy 421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633
Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693
Qy 541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753
Qy 601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813
Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
Db 814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873
Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933
Qy 781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
Db 934 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993
Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

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Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1234 CTCAGTGGC 1242
```

RESULT 6
AAF32103
ID AAF32103 standard; cDNA; 1564 BP.
XX
AC AAF32103;
XX
DT 10-APR-2001 (first entry)
XX
DE Human HFGAN72 receptor coding sequence SEQ ID NO: 12.
XX
KW Human; mouse; rat; Lig72A; Lig72B; neuropeptide receptor; HFGAN72;
KW truncation mutant; ligand; neurodegenerative disorder; pain;
KW eating disorder; behaviour disorder; mood disorder; ss.
XX
OS Homo sapiens.
XX
PN WO200100787-A2.
XX
PD 04-JAN-2001.
XX
PF 22-JUN-2000; 2000WO-US017251.
XX
PR 25-JUN-1999; 99US-0141156P.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
PA (SMIK) SMITHKLINE BEECHAM PLC.
XX
PI Bingham S, Darker J, Liu W, Martin JD, Parsons AA, Patel SR;
XX
DR WPI; 2001-071483/08.
XX
PT Polynucleotides encoding Lig 72A polypeptides or their variants, which
PT are useful in the treatment of a disease or disorder associated with
PT pain, e.g. enhanced or exaggerated sensitivity to pain, hyperalgesia,
PT neuropathic pain and back pain.
XX
PS Disclosure; Fig 6; 101pp; English.
XX
CC The present invention provides the protein and coding sequences for the
CC human, mouse and rat HFGAN receptor ligand Lig72A. It also provides
CC truncated mutant versions. These, and their agonists and antagonists, are
CC all useful in the treatment of eating, neurodegenerative, behaviour,
CC mood, sexual, hormonal and sleep disorders, pain, depression, epilepsy
CC and acute inflammatory conditions

XX
SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 97.2%; Score 1079.4; DB 4; Length 1564;
Best Local Similarity 99.4%; Pred. No. 8.9e-246;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1234 CTCAGTGGC 1242
```

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RESULT 7
ABA96021
ID   ABA96021 standard; cDNA; 1564 BP.
XX
AC   ABA96021;
XX
DT   12-MAR-2002  (first entry)
XX
DE   HGS EST 554692.
XX
KW   G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW   nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW   infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW   cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW   benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW   schizophrenia; manic depression; dementia; mental retardation; EST;
KW   dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;
KW   HGS EST 554692; expressed sequence tag; probe; ss.
XX
OS   Homo sapiens.
XX
PN   EP1156110-A2.
XX
PD   21-NOV-2001.
XX
PF   27-OCT-1997; 2001EP-00203010.
XX
PR   30-APR-1997;   97US-00846705.
PR   27-OCT-1997;   97EP-00308554.
XX
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PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 2002-084320/12.
XX
PT New polynucleotide encoding a G-protein coupled receptor designated
PT HFGAN72Y is useful to diagnose and treat associated diseases including
PT cancer, infection, cardiac disease and psychotic and neurological
PT disorders.
XX
PS Example 1; Page 19-20; 22pp; English.
XX
CC The sequence represents HGS EST 554692. The sequence was used in the
CC invention as a probe to screen a human genomic placenta phage library.
CC The invention relates to a novel isolated polynucleotide encoding
CC HFGAN72Y polypeptide. The polypeptide of the invention has cytostatic,
CC cardiant, analgesic, tranquillising, nootropic, neuroprotective, and anti
CC -asthmatic activity. The HFGAN72Y has a use in gene therapy. The HFGAN72Y
CC polynucleotide or an HFGAN72Y polypeptide agonist are used to treat a
CC subject in need of enhanced HFGAN72Y activity or expression. An HFGAN72Y
CC antagonist or competitor, or nucleic acid which inhibits HFGAN72Y
CC expression is used to treat a subject in need of decreased HFGAN72Y
CC activity or expression. HFGAN72Y-associated diseases include infections,
CC particularly by HIV-1 or HIV-2, pain, anorexia, bulimia, Parkinson's
CC disease, cardiac diseases, cancers, ulcers, urinary retention, asthma,
CC allergies, benign prostatic hypertrophy, and psychotic and neurological
CC disorders including anxiety, schizophrenia, manic depression, delirium,
CC dementia, severe mental retardation and dyskinesias such as Huntington's
CC disease and Tourette's syndrome
XX
SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 97.2%; Score 1079.4; DB 6; Length 1564;
Best Local Similarity 99.4%; Pred. No. 8.9e-246;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453
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Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||||  ||| ||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1234 CTCAGTGGC 1242
```

RESULT 8
AAI64173
ID AAI64173 standard; cDNA; 1564 BP.
XX
AC AAI64173;
XX
DT 22-JAN-2002 (first entry)
XX
DE HFGAN72X G coupled receptor polypeptide partial sequence.
XX
KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;
KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;
KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; probe;
KW myocardial infarction; ulcers; asthma; allergy; delirium; dementia;
KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor; ss.
XX
OS Homo sapiens.
XX
FH Key   Location/Qualifiers
FT CDS   154. .1362
FT   /*tag= a
FT   /partial
FT   /product= "HFGAN72X protein"
FT   /note= "The specification states that this is a partial
FT   sequence even though it contains start and stop codons;
FT   HFGAN72X is a G coupled receptor polypeptide"
FT   /transl_except= (pos:991. .993, aa:Ala)
XX
PN EP1154019-A2.
XX
PD 14-NOV-2001.
XX
PF 27-OCT-1997; 2001EP-00203008.
XX
PR 30-APR-1997; 97US-00846704.
PR 27-OCT-1997; 97EP-00308563.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 2002-012659/02.
DR P-PSDB; AAG78346.
XX
PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
PT disease, and acute heart failure.
XX
PS Example 3; Page 9; 24pp; English.
XX
CC The present sequence is that of a known partial nucleotide sequence
CC encoding a HFGAN72X polypeptide (AAG78346) used as a probe to identify
CC the HFGAN72X gene (AAI64173). The specification describes a newly

CC isolated polynucleotide encoding a human HFGAN72X G coupled receptor
CC polypeptide. The protein of the invention has antibacterial, fungicide,
CC virucide, protozoacide, anti-HIV, cardiant, analgesic, cytostatic,
CC nootropic, antiparkinsonian, antiulcer, antiasthmatic, tranquiliser,
CC neuroleptic, antidepressant, anticonvulsant and osteopathic activities.
CC HFGAN72X polynucleotides (PNs) are used to express HFGAN72X in vivo, to
CC treat diseases requiring increased activity or expression of HFGAN72X;
CC for recombinant production of HFGAN72X; diagnose diseases by detecting
CC mutations in genomic sequences and in chromosome identification and
CC mapping. HFGAN72X polypeptides are used to raise specific antibodies; as
CC therapeutic agents; to identify HFGAN72X protein-expressing clones; to
CC purify HFGAN72X proteins; in vaccines. Cells transformed with HFGAN72X
CC PNs are used to identify (ant)agonists of HFGAN72X, useful
CC therapeutically. Nucleic acids that inhibit expression of HFGAN72X and
CC polypeptides that compete with ligands for binding to HFGAN72X proteins
CC are also useful therapeutically and diagnostically. HFGAN72X-related
CC diseases include infections (bacterial, viral, fungal or protozoal,
CC particularly HIV-1 or -2); pain; cancer; anorexia; bulimia; Parkinson's
CC disease; acute heart failure; hypotension; hypertension; urinary
CC retention; osteoporosis; angina pectoris; myocardial infarction; ulcers;
CC asthma; allergy; benign prostatic hypertrophy; anxiety; schizophrenia;
CC manic depression; delirium; dementia; severe mental retardation and
CC dyskinesias
XX
SQ Sequence 1564 BP; 269 A; 508 C; 436 G; 347 T; 0 U; 4 Other;

Query Match 97.2%; Score 1079.4; DB 6; Length 1564;
Best Local Similarity 99.4%; Pred. No. 8.9e-246;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Db        934 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1234 CTCAGTGGC 1242
```

RESULT 9
AAI64172
ID AAI64172 standard; cDNA; 1564 BP.
XX
AC AAI64172;
XX
DT 22-JAN-2002 (first entry)

XX
DE Human HFGAN72X G coupled receptor polypeptide cDNA.
XX
KW Antibacterial; fungicide; virucide; protozoacide; anti-HIV; analgesic;
KW cytostatic; nootropic; antiparkinsonian; cardiant; antiulcer;
KW antiasthmatic; tranquiliser; neuroleptic; antidepressant; anticonvulsant;
KW osteopathic; HIV infection; pain; cancer; anorexia; bulimia;
KW Parkinson's disease; acute heart failure; hypotension; hypertension;
KW urinary retention; osteoporosis; angina pectoris; myocardial infarction;
KW ulcers; asthma; allergy; delirium; dementia;
KW benign prostatic hypertrophy; anxiety; schizophrenia; manic depression;
KW dyskinesia; G coupled receptor; HFGAN72X; 7 transmembrane receptor; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 154. .1431
FT /*tag= a
FT /product= "HFGAN72X protein"
FT /note= "G coupled receptor polypeptide"
XX
PN EP1154019-A2.
XX
PD 14-NOV-2001.
XX
PF 27-OCT-1997; 2001EP-00203008.
XX
PR 30-APR-1997; 97US-00846704.
PR 27-OCT-1997; 97EP-00308563.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 2002-012659/02.
DR P-PSDB; AAG78345.
XX
PT Nucleic acid encoding the HFGAN72X receptor, useful for diagnosis and
PT treatment of e.g. infections, cancer, anorexia, bulimia, Parkinson's
PT disease, and acute heart failure.
XX
PS Claim 3; Page 7; 24pp; English.
XX
CC The present sequence is that of a cDNA encoding a HFGAN72X polypeptide
CC (AAG78345). The specification describes a newly isolated polynucleotide
CC encoding a HFGAN72X G coupled receptor polypeptide. The protein of the
CC invention has antibacterial, fungicide, virucide, protozoacide, anti-HIV,
CC cardiant, analgesic, cytostatic, nootropic, antiparkinsonian, antiulcer,
CC antiasthmatic, tranquiliser, neuroleptic, antidepressant, anticonvulsant
CC and osteopathic activities. HFGAN72X polynucleotides (PNs) are used to
CC express HFGAN72X in vivo, to treat diseases requiring increased activity
CC or expression of HFGAN72X; for recombinant production of HFGAN72X;
CC diagnose diseases (or susceptibility to them) by detecting mutations in
CC genomic sequences and in chromosome identification and mapping. HFGAN72X
CC polypeptides are used to raise specific antibodies; as therapeutic agents
CC ; to identify HFGAN72X protein-expressing clones; to purify HFGAN72X
CC proteins; in vaccines. Cells transformed with HFGAN72X PNs are used to

CC identify (ant)agonists of HFGAN72X, useful therapeutically. Nucleic acids
CC that inhibit expression of HFGAN72X and polypeptides that compete with
CC ligands for binding to HFGAN72X proteins are also useful therapeutically
CC and diagnostically. HFGAN72X-related diseases include infections
CC (bacterial, viral, fungal or protozoal, particularly HIV-1 or -2); pain;
CC cancer; anorexia; bulimia; Parkinson's disease; acute heart failure;
CC hypotension; hypertension; urinary retention; osteoporosis; angina
CC pectoris; myocardial infarction; ulcers; asthma; allergy; benign
CC prostatic hypertrophy; anxiety; schizophrenia; manic depression; delirium
CC ; dementia; severe mental retardation and dyskinesias
XX
SQ Sequence 1564 BP; 271 A; 511 C; 435 G; 347 T; 0 U; 0 Other;

Query Match 97.2%; Score 1079.4; DB 6; Length 1564;
Best Local Similarity 99.4%; Pred. No. 8.9e-246;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753
```

```
Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1234 CTCAGTGGC 1242
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RESULT 10
ABZ42789
ID ABZ42789 standard; DNA; 1564 BP.
XX
AC ABZ42789;
XX
DT 04-MAR-2003 (first entry)
XX
DE Human orexin receptor 1 nucleotide SEQ ID NO:367.
XX
KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;
KW G protein-coupled receptor modulator; antibody; immune-related disease;
KW growth-related disease; cell regeneration-related disease; AIDS; cancer;
KW immunological-related cell proliferative disease; autoimmune disease;
KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;
KW osteoporosis; cardiomyopathy; inflammation; Crohn's disease; diabetes;
KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;
KW psoriasis; anxiety; depression; schizophrenia; dementia; memory loss;
KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;
KW hypertension; hypotension; renal disorder; rheumatoid arthritis; trauma;

KW ulcer; gene; ds.
XX
OS Homo sapiens.
XX
PN WO200261087-A2.
XX
PD 08-AUG-2002.
XX
PF 19-DEC-2001; 2001WO-US050107.
XX
PR 19-DEC-2000; 2000US-0257144P.
XX
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
XX
PI Burmer GC, Roush CL, Brown JP;
XX
DR WPI; 2003-046718/04.
DR P-PSDB; ABP81941.
XX
PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.
XX
PS Disclosure; Fig 1; 523pp; English.
XX
CC The present invention describes antigenic peptides (I) comprising: (a)
CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
CC acids. Also described: (1) an assay for the detection of a particular G
CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
CC and (2) an isolated antibody having high specificity and high affinity or
CC avidity for a particular GPCR. (I) can be used as GPCR modulators and in
CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
CC antibody against a particular GPCR, and in the production of specific
CC antibodies. The peptides and antibodies are also useful for detecting the
CC presence or absence of corresponding GPCRs. The antigenic peptides for
CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC treating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 1564 BP; 268 A; 513 C; 436 G; 347 T; 0 U; 0 Other;

Query Match 97.2%; Score 1079.4; DB 7; Length 1564;
Best Local Similarity 99.4%; Pred. No. 8.9e-246;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy        1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy       61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy      121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy      181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy      241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy      301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy      361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy      421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy      481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy      541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db      694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy      601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy      661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy      721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy      781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      934 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993
```

```
Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1234 CTCAGTGGC 1242
```

RESULT 11
AAV68512
ID AAV68512 standard; cDNA; 1133 BP.
XX
AC AAV68512;
XX
DT 29-JAN-1999 (first entry)
XX
DE Nucleotide sequence of HGS EST 557082.
XX
KW HGS EST 557082; G-protein coupled receptor family; HFGAN72Y; mutation;
KW probe; agonist; antagonist; activation; inhibition; gene therapy;
KW antibody; immune response; vaccine; HIV-1; HIV-2; cancer; anorexia;
KW bulimia; asthma; Parkinson's disease; acute heart failure; hypotension;
KW hypertension; urinary retention; osteoporosis; angina pectoris;
KW myocardial infarction; ulcer; allergies; psychotic disorder;
KW neurological disorder; gene mapping; ss.
XX
OS Homo sapiens.
XX
PN EP875565-A2.
XX
PD 04-NOV-1998.
XX
PF 27-OCT-1997; 97EP-00308554.
XX
PR 30-APR-1997; 97US-00846705.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis C;
XX
DR WPI; 1998-570286/49.
XX
PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of HIV

PT infections, cancer, osteoporosis and Parkinson's disease.
XX
PS Example 1; Page 18-19; 22pp; English.
XX
CC This is the nucleotide sequence of the HGS EST 557082 used in the method
CC of the invention involving the G-protein coupled receptor, HFGAN72Y. Its
CC polypeptides and polynucleotides are useful for diagnosing susceptibility
CC to diseases by detecting mutations in the HFGAN72Y gene using probes
CC containing the HFGAN72Y nucleotide sequence, and can diagnose diseases
CC associated with HFGAN72Y imbalance by determining HFGAN72Y polypeptide or
CC mRNA expression levels. Agonists/antagonists can be used in treatment to
CC activate/inhibit HFGAN72Y activity, in addition to direct administration
CC of antisense sequences to prevent expression, or HFGAN72Y polypeptides to
CC treat conditions associated with a lack HFGAN72Y protein. Gene therapy
CC may also be used to affect endogenous HFGAN72Y polypeptide production.
CC HFGAN72Y antibodies are useful for inducing an immune response to
CC immunise and prevent diseases, and for isolating HFGAN72Y clones or
CC purifying the polypeptides by affinity chromatography. HFGAN72Y
CC polypeptides can be administered directly or as a vaccine to inoculate
CC against diseases. Diseases diagnosed, prevented or treated include HIV-1
CC or HIV-2 infections, pain, cancers, anorexia, bulimia, asthma,
CC Parkinson's disease, acute heart failure, hypotension, hypertension,
CC urinary retention, osteoporosis, angina pectoris, myocardial infarction,
CC ulcers; allergies, benign prostatic hypertrophy, and psychotic and
CC neurological disorders. The HFGAN72Y polypeptide is also useful for
CC mapping the gene to a chromosome, allowing gene inheritance to be studied
CC through linkage analysis
XX
SQ Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

Query Match 97.2%; Score 1078.4; DB 2; Length 1133;
Best Local Similarity 99.4%; Pred. No. 1.4e-245;
Matches 1082; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
```

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Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||||  ||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
```

RESULT 12
ABA96020
ID ABA96020 standard; cDNA; 1133 BP.

XX
AC ABA96020;
XX
DT 12-MAR-2002 (first entry)
XX
DE HGS EST 557082.
XX
KW G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW schizophrenia; manic depression; dementia; mental retardation; EST;
KW dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2;
KW HGS EST 557082; expressed sequence tag; ss.
XX
OS Homo sapiens.
XX
PN EP1156110-A2.
XX
PD 21-NOV-2001.
XX
PF 27-OCT-1997; 2001EP-00203010.
XX
PR 30-APR-1997; 97US-00846705.
PR 27-OCT-1997; 97EP-00308554.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis CE;
XX
DR WPI; 2002-084320/12.
XX
PT New polynucleotide encoding a G-protein coupled receptor designated
PT HFGAN72Y is useful to diagnose and treat associated diseases including
PT cancer, infection, cardiac disease and psychotic and neurological
PT disorders.
XX
PS Example 1; Page 18-19; 22pp; English.
XX
CC The sequence represents HGS EST 557082. The invention relates to a novel
CC isolated polynucleotide encoding HFGAN72Y polypeptide. The polypeptide of
CC the invention has cytostatic, cardiant, analgesic, tranquillising,
CC nootropic, neuroprotective, and anti-asthmatic activity. The HFGAN72Y has
CC a use in gene therapy. The HFGAN72Y polynucleotide or an HFGAN72Y
CC polypeptide agonist are used to treat a subject in need of enhanced
CC HFGAN72Y activity or expression. An HFGAN72Y antagonist or competitor, or
CC nucleic acid which inhibits HFGAN72Y expression is used to treat a
CC subject in need of decreased HFGAN72Y activity or expression. HFGAN72Y-
CC associated diseases include infections, particularly by HIV-1 or HIV-2,
CC pain, anorexia, bulimia, Parkinson's disease, cardiac diseases, cancers,
CC ulcers, urinary retention, asthma, allergies, benign prostatic
CC hypertrophy, and psychotic and neurological disorders including anxiety,
CC schizophrenia, manic depression, delirium, dementia, severe mental
CC retardation and dyskinesias such as Huntington's disease and Tourette's
CC syndrome
XX

SQ Sequence 1133 BP; 202 A; 366 C; 314 G; 251 T; 0 U; 0 Other;

Query Match 97.2%; Score 1078.4; DB 6; Length 1133;
Best Local Similarity 99.4%; Pred. No. 1.4e-245;
Matches 1082; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
```

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Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
```

```
RESULT 13
AAV68511
ID   AAV68511 standard; cDNA; 1170 BP.
XX
AC   AAV68511;
XX
DT   29-JAN-1999  (first entry)
XX
DE   Nucleotide sequence of HFGAN72Y a G-protein coupled receptor.
XX
KW   G-protein coupled receptor family; HFGAN72Y; mutation; probe; agonist;
KW   antagonist; activation; inhibition; gene therapy; antibody;
KW   immune response; vaccine; HIV-1; HIV-2; cancer; anorexia; bulimia;
KW   asthma; Parkinson's disease; acute heart failure; hypotension;
KW   hypertension; urinary retention; osteoporosis; angina pectoris;
KW   myocardial infarction; ulcer; allergies; psychotic disorder;
KW   neurological disorder; gene mapping; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1170
FT                   /*tag=  a
FT                   /product= "HFGAN72Y protein"
XX
PN   EP875565-A2.
XX
PD   04-NOV-1998.
XX
PF   27-OCT-1997;   97EP-00308554.
XX
```

PR 30-APR-1997; 97US-00846705.
XX
PA (SMIK) SMITHKLINE BEECHAM CORP.
XX
PI Bergsma DJ, Ellis C;
XX
DR WPI; 1998-570286/49.
DR P-PSDB; AAW80805.
XX
PT New G-protein coupled receptor HFGAN72Y polypeptide and polynucleotide -
PT useful as diagnostic reagents and for prevention and treatment of HIV
PT infections, cancer, osteoporosis and Parkinson's disease.
XX
PS Claim 3; Page 7; 22pp; English.
XX
CC This is the nucleotide sequence of the G-protein coupled receptor,
CC HFGAN72Y used in the method of the invention. HFGAN72Y polypeptides and
CC polynucleotides are useful for diagnosing susceptibility to diseases by
CC detecting mutations in the HFGAN72Y gene using probes containing the
CC HFGAN72Y nucleotide sequence, and can diagnose diseases associated with
CC HFGAN72Y imbalance by determining HFGAN72Y polypeptide or mRNA expression
CC levels. Agonists/antagonists can be used in treatment to activate/inhibit
CC HFGAN72Y activity, in addition to direct administration of antisense
CC sequences to prevent expression, or HFGAN72Y polypeptides to treat
CC conditions associated with a lack HFGAN72Y protein. Gene therapy may also
CC be used to affect endogenous HFGAN72Y polypeptide production. HFGAN72Y
CC antibodies are useful for inducing an immune response to immunise and
CC prevent diseases, and for isolating HFGAN72Y clones or purifying the
CC polypeptides by affinity chromatography. HFGAN72Y polypeptides can be
CC administered directly or as a vaccine to inoculate against diseases.
CC Diseases diagnosed, prevented or treated include HIV-1 or HIV-2
CC infections, pain, cancers, anorexia, bulimia, asthma, Parkinson's
CC disease, acute heart failure, hypotension, hypertension, urinary
CC retention, osteoporosis, angina pectoris, myocardial infarction, ulcers;
CC allergies, benign prostatic hypertrophy, and psychotic and neurological
CC disorders. The HFGAN72Y polypeptide is also useful for mapping the gene
CC to a chromosome, allowing gene inheritance to be studied through linkage
CC analysis
XX
SQ Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

Query Match 97.2%; Score 1078.4; DB 2; Length 1170;
Best Local Similarity 99.4%; Pred. No. 1.4e-245;
Matches 1082; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

```
Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
```

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Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
                    ||||||||
Db       1081 CTCAGTGG 1088


RESULT 14
ABA96019
ID   ABA96019 standard; cDNA; 1170 BP.
XX
AC   ABA96019;
XX
DT   12-MAR-2002  (first entry)
XX
DE   G-protein coupled receptor (HFGAN72Y) cDNA.
XX
KW   G-protein; receptor; HFGAN72Y; cytostatic; cardiant; analgesic; cancer;
KW   nootropic; tranquillising; neuroprotective; anti-asthmatic; gene therapy;
KW   infection; HIV-1; pain; anorexia; bulimia; Parkinson's disease; ulcer;
KW   cardiac disease; urinary retention; asthma; allergy; psychotic disorder;
KW   benign prostatic hypertrophy; neurological disorder; anxiety; delirium;
KW   schizophrenia; manic depression; dementia; mental retardation;
KW   dyskinesia; Huntington's disease; Tourette's syndrome; HIV-2; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .1170
FT                   /*tag=  a
FT                   /product= "HGFAN72Y"
XX
PN   EP1156110-A2.
XX
PD   21-NOV-2001.
XX
PF   27-OCT-1997; 2001EP-00203010.
XX
PR   30-APR-1997;   97US-00846705.
PR   27-OCT-1997;   97EP-00308554.
XX
PA   (SMIK ) SMITHKLINE BEECHAM CORP.
XX
PI   Bergsma DJ,  Ellis CE;
XX
DR   WPI; 2002-084320/12.
DR   P-PSDB; ABB08208.
XX
PT   New polynucleotide encoding a G-protein coupled receptor designated
PT   HFGAN72Y is useful to diagnose and treat associated diseases including
PT   cancer, infection, cardiac disease and psychotic and neurological
PT   disorders.
XX
PS   Claim 3; Page 7; 22pp; English.
XX
CC   The sequence encodes G-protein coupled receptor HFGAN72Y. The invention
```

CC relates to a novel isolated polynucleotide encoding HFGAN72Y polypeptide.
CC The polypeptide of the invention has cytostatic, cardiant, analgesic,
CC tranquillising, nootropic, neuroprotective, and anti-asthmatic activity.
CC The HFGAN72Y has a use in gene therapy. The HFGAN72Y polynucleotide or an
CC HFGAN72Y polypeptide agonist are used to treat a subject in need of
CC enhanced HFGAN72Y activity or expression. An HFGAN72Y antagonist or
CC competitor, or nucleic acid which inhibits HFGAN72Y expression is used to
CC treat a subject in need of decreased HFGAN72Y activity or expression.
CC HFGAN72Y-associated diseases include infections, particularly by HIV-1 or
CC HIV-2, pain, anorexia, bulimia, Parkinson's disease, cardiac diseases,
CC cancers, ulcers, urinary retention, asthma, allergies, benign prostatic
CC hypertrophy, and psychotic and neurological disorders including anxiety,
CC schizophrenia, manic depression, delirium, dementia, severe mental
CC retardation and dyskinesias such as Huntington's disease and Tourette's
CC syndrome
XX
SQ Sequence 1170 BP; 208 A; 381 C; 322 G; 259 T; 0 U; 0 Other;

Query Match 97.2%; Score 1078.4; DB 6; Length 1170;
Best Local Similarity 99.4%; Pred. No. 1.4e-245;
Matches 1082; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
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Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
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RESULT 15
AAS00491
ID   AAS00491 standard; cDNA; 1278 BP.
XX
AC   AAS00491;
XX
DT   17-MAY-2001  (first entry)
XX
DE   Human neuropeptide receptor cDNA.
XX
KW   Human; neuropeptide receptor; neuropeptide Y receptor; obesity;
KW   nervous system disorder; hyperproliferative disorder; diabetes mellitus;
KW   cardiovascular disorder; autoimmune disorder; infectious disorder;
KW   eating behaviour disorder; narcolepsy; neurological disease;
KW   narcotics addiction; nicotine addiction; alcohol addiction; gene therapy;
```

KW protein co-ordinate data; chromosome 1; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .1278
FT /*tag= a
FT /product= "neuropeptide receptor"
XX
PN WO200117532-A1.
XX
PD 15-MAR-2001.
XX
PF 07-SEP-2000; 2000WO-US024518.
XX
PR 10-SEP-1999; 99US-00393696.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Soppet DR, Li Y, Rosen CA;
XX
DR WPI; 2001-183276/18.
DR P-PSDB; AAU00438.
XX
PT A new nucleic acid encoding a human neuropeptide receptor polypeptide,
PT useful for preventing, treating or ameliorating obesity, narcolepsy,
PT neurological disease and addiction to narcotics, nicotine and alcohol.
XX
PS Claim 4; Fig 1; 385pp; English.
XX
CC The present sequence encodes for a novel human neuropeptide receptor
CC which shows sequence homology to the neuropeptide Y receptor. Two splice
CC variants of the neuropeptide receptor (AAU00439-AAU00440) and a possible
CC mutant (AAU00442) are also described. Polypeptides and polynucleotides of
CC the neuropeptide receptor are useful for diagnosing, preventing, or
CC treating a pathological condition in a subject related to the central
CC nervous and peripheral nervous systems (CNS and PNS). The polypeptides
CC and polynucleotides may be used to treat hyperproliferative,
CC cardiovascular, autoimmune, nervous system or infectious disorders e.g.
CC cancer, heart disease, rheumatoid arthritis, Alzheimer's disease, HIV
CC infection and diabetes mellitus. In particular they are useful for
CC preventing, treating or ameliorating a medical condition in a mammal such
CC as obesity/eating behaviour disorders, narcolepsy, neurological disease,
CC addiction to narcotics, nicotine and alcohol, chronic pain, acute pain,
CC migraine headaches and anxiety disorders. The polynucleotides encoding
CC the neuropeptide receptor can also be used in gene therapy methods for
CC treating such diseases
XX
SQ Sequence 1278 BP; 220 A; 426 C; 347 G; 285 T; 0 U; 0 Other;

Query Match 97.1%; Score 1077.8; DB 4; Length 1278;
Best Local Similarity 99.4%; Pred. No. 2e-245;
Matches 1082; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

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Qy        61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy       421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy       541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
             |||||||||  |||  ||||||||||||||||||||||||||||||||||||||||||||
Db       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy       601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGCC 840

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy       1081 CTCAGTGGC 1089
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Db       1081 CTCAGTGGC 1089
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1110	100.0	1110	5	PCT-US95-05616-3	Sequence 3, Appli
2	1102	99.3	1110	4	US-08-462-509B-3	Sequence 3, Appli
3	1079.4	97.2	1209	4	US-08-462-509B-1	Sequence 1, Appli
4	1079.4	97.2	1564	2	US-08-846-705-4	Sequence 4, Appli
5	1079.4	97.2	1564	3	US-08-846-704-1	Sequence 1, Appli
6	1079.4	97.2	1564	3	US-08-846-704-3	Sequence 3, Appli
7	1078.4	97.2	1133	2	US-08-846-705-3	Sequence 3, Appli
8	1078.4	97.2	1170	2	US-08-846-705-1	Sequence 1, Appli
9	1077.8	97.1	1209	5	PCT-US95-05616-1	Sequence 1, Appli
10	1075.2	96.9	1116	4	US-08-462-509B-5	Sequence 5, Appli
11	1075.2	96.9	1133	5	PCT-US95-05616-5	Sequence 5, Appli

12	688	62.0	843	3	US-08-513-974B-375	Sequence 375, App
13	661	59.5	789	3	US-08-513-974B-55	Sequence 55, Appl
14	661	59.5	789	4	US-09-461-436B-55	Sequence 55, Appl
15	511.8	46.1	1633	3	US-09-119-788-1	Sequence 1, Appli
16	241.2	21.7	9785	4	US-09-479-128-1	Sequence 1, Appli
17	161.6	14.6	1293	3	US-09-255-368-7	Sequence 7, Appli
18	154.6	13.9	1410	3	US-09-255-368-1	Sequence 1, Appli
19	120.4	10.8	168575	4	US-09-426-290-1	Sequence 1, Appli
20	117.4	10.6	1110	3	US-08-513-974B-31	Sequence 31, Appl
21	117.4	10.6	1110	3	US-08-776-971-26	Sequence 26, Appl
22	117.4	10.6	1110	4	US-09-461-436B-31	Sequence 31, Appl
23	117.4	10.6	1331	3	US-08-513-974B-322	Sequence 322, App
24	117.4	10.6	1331	3	US-08-776-971-103	Sequence 103, App
25	108.8	9.8	1113	3	US-09-172-353-1	Sequence 1, Appli
26	108.8	9.8	1113	4	US-09-799-955-1	Sequence 1, Appli
27	107.2	9.7	669	3	US-08-513-974B-314	Sequence 314, App
28	107.2	9.7	669	3	US-08-776-971-99	Sequence 99, Appl
29	101.6	9.2	1110	4	US-09-170-496D-25	Sequence 25, Appl
30	101.6	9.2	1110	4	US-09-170-496D-177	Sequence 177, App
31	101.6	9.2	1344	4	US-09-016-434-1295	Sequence 1295, Ap
32	101.6	9.2	1356	1	US-07-978-892A-4	Sequence 4, Appli
33	101.6	9.2	1535	4	US-09-016-434-1051	Sequence 1051, Ap
34	101.6	9.2	1969	1	US-07-937-609-28	Sequence 28, Appl
35	101.6	9.2	1969	3	US-08-029-170-28	Sequence 28, Appl
36	98.4	8.9	1621	1	US-08-722-001-13	Sequence 13, Appl
37	98.4	8.9	1776	1	US-08-722-001-29	Sequence 29, Appl
38	98.4	8.9	2002	4	US-09-016-434-1172	Sequence 1172, Ap
39	98.4	8.9	2140	1	US-08-334-698-1	Sequence 1, Appli
40	98.4	8.9	2140	1	US-08-228-932-1	Sequence 1, Appli
41	98.4	8.9	2140	1	US-08-468-939-1	Sequence 1, Appli
42	98.4	8.9	2140	2	US-08-406-855A-1	Sequence 1, Appli
43	98.4	8.9	2140	2	US-08-722-190-1	Sequence 1, Appli
44	98.4	8.9	2140	3	US-08-244-354-1	Sequence 1, Appli
45	98.4	8.9	2140	3	US-09-206-899-1	Sequence 1, Appli

ALIGNMENTS

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RESULT 1
PCT-US95-05616-3
; Sequence 3, Application PC/TUS9505616
;  GENERAL INFORMATION:
;    APPLICANT:  LI, ET AL.
;    TITLE OF INVENTION:  Human Neuropeptide Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
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;       OPERATING SYSTEM:  MS-DOS
;       SOFTWARE:  WORD PERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/05616
;       FILING DATE:  concurrently
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FERRARO, GREGORY D.
;       REGISTRATION NUMBER:  36,134
;       REFERENCE/DOCKET NUMBER:  325800-268
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1110 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  cDNA
PCT-US95-05616-3

  Query Match             100.0%;  Score 1110;  DB 5;  Length 1110;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-255;
  Matches 1110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
              |||||||||||||||||||||||||||||
Db       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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RESULT 2
US-08-462-509B-3
; Sequence 3, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue

```
;       CITY:  Rockiville
;       STATE:  MD
;       COUNTRY:  USA
;       ZIP:  20850
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/462,509B
;       FILING DATE:  05-JUN-1995
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  WO PCT/US95/05616
;       FILING DATE:  05-MAY-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Wales, Michele M.
;       REGISTRATION NUMBER:  43,975
;       REFERENCE/DOCKET NUMBER:  PF168P1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  301-309-8504
;       TELEFAX:  301-309-8439
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1110 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  1..1110
US-08-462-509B-3

  Query Match             99.3%;  Score 1102;  DB 4;  Length 1110;
  Best Local Similarity   99.5%;  Pred. No. 3.3e-253;
  Matches 1105;  Conservative    0;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
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Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
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Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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Db       1081 CTCAGTGGCCTTCCCTGGAGTCTGCTCTAA 1110
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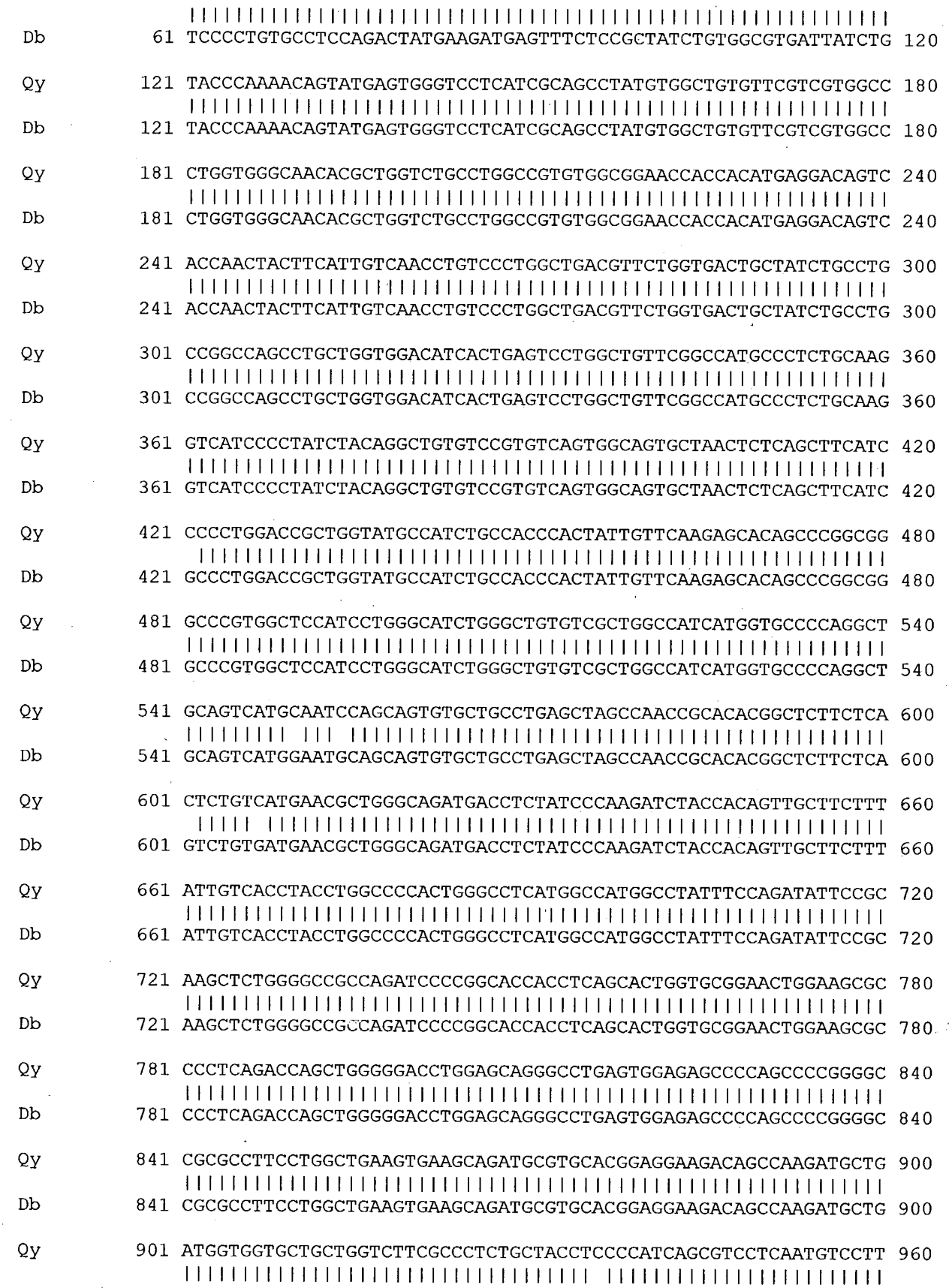
RESULT 3
US-08-462-509B-1
; Sequence 1, Application US/08462509B
; Patent No. 6410701
; GENERAL INFORMATION:
;   APPLICANT: Soppet, Daniel et al
;   TITLE OF INVENTION: Human Neuropeptide Receptor
;   NUMBER OF SEQUENCES: 12
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Human Genome Sciences, Inc.
;   STREET: 9410 Key West Avenue
;   CITY: Rockiville
;   STATE: MD
;   COUNTRY: USA
;   ZIP: 20850
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/462,509B
;   FILING DATE: 05-JUN-1995
;   CLASSIFICATION: 435
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: WO PCT/US95/05616
;   FILING DATE: 05-MAY-1995
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wales, Michele M.
;   REGISTRATION NUMBER: 43,975
;   REFERENCE/DOCKET NUMBER: PF168P1
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 301-309-8504
;   TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 1209 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: DNA (genomic)
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1..1209
US-08-462-509B-1

  Query Match 97.2%; Score 1079.4; DB 4; Length 1209;
  Best Local Similarity 99.4%; Pred. No. 8.1e-248;
  Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
      ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy 61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120



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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1081 CTCAGTGGC 1089
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RESULT 4
US-08-846-705-4
; Sequence 4, Application US/08846705
; Patent No. 5935814
;  GENERAL INFORMATION:
;    APPLICANT:  BERGSMA, DERK J.
;    APPLICANT:  ELLIS, CATHERINE E
;    TITLE OF INVENTION:  NOVEL G-PROTEIN COUPLED
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,705
;      FILING DATE:  30-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-70003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1564 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
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; MOLECULE TYPE: cDNA
US-08-846-705-4

Query Match 97.2%; Score 1079.4; DB 2; Length 1564;
Best Local Similarity 99.4%; Pred. No. 8.7e-248;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||||  ||| ||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1234 CTCAGTGGC 1242


RESULT 5
US-08-846-704-1
; Sequence 1, Application US/08846704
; Patent No. 6020157
;  GENERAL INFORMATION:
;    APPLICANT:  BERGSMA, DERK J.
;    APPLICANT:  ELLIS, CATHERINE E.
;    TITLE OF INVENTION:  NOVEL G-PROTEIN COUPLED
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,704
;      FILING DATE:  30-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
```

; REGISTRATION NUMBER: 23,031
; REFERENCE/DOCKET NUMBER: GH-70002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-407-0700
; TELEFAX: 610-407-0701
; TELEX: 846169
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1564 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-846-704-1

Query Match 97.2%; Score 1079.4; DB 3; Length 1564;
Best Local Similarity 99.4%; Pred. No. 8.7e-248;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||||  ||| ||||||||||||||||||||||||||||||||||||||||||||
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Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
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Db       1234 CTCAGTGGC 1242
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RESULT 6
US-08-846-704-3
; Sequence 3, Application US/08846704
; Patent No. 6020157
;  GENERAL INFORMATION:
;    APPLICANT:  BERGSMA, DERK J.
;    APPLICANT:  ELLIS, CATHERINE E.
;    TITLE OF INVENTION:  NOVEL G-PROTEIN COUPLED
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
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;       COMPUTER:  IBM Compatible
;       OPERATING SYSTEM:  DOS
;       SOFTWARE:  FastSEQ for Windows Version 2.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/846,704
;       FILING DATE:  30-APR-1997
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:
;       FILING DATE:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  PRESTIA, PAUL F
;       REGISTRATION NUMBER:  23,031
;       REFERENCE/DOCKET NUMBER:  GH-70002
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  610-407-0700
;       TELEFAX:  610-407-0701
;       TELEX:  846169
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1564 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-846-704-3

  Query Match             97.2%;  Score 1079.4;  DB 3;  Length 1564;
  Best Local Similarity   99.4%;  Pred. No. 8.7e-248;
  Matches 1083;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
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Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||||  ||| ||||||||||||||||||||||||||||||||||||||||||||
Db        694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db       1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1234 CTCAGTGGC 1242
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RESULT 7
US-08-846-705-3
; Sequence 3, Application US/08846705
; Patent No. 5935814
; GENERAL INFORMATION:
; APPLICANT: BERGSMA, DERK J.

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;    APPLICANT:  ELLIS, CATHERINE E
;    TITLE OF INVENTION:  NOVEL G-PROTEIN COUPLED
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,705
;      FILING DATE:  30-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-70003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1133 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-846-705-3

  Query Match             97.2%;  Score 1078.4;  DB 2;  Length 1133;
  Best Local Similarity   99.4%;  Pred. No. 1.4e-247;
  Matches 1082;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||||  ||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088


RESULT 8
US-08-846-705-1
; Sequence 1, Application US/08846705
; Patent No. 5935814
;  GENERAL INFORMATION:
;    APPLICANT:  BERGSMA, DERK J.
;    APPLICANT:  ELLIS, CATHERINE E
;    TITLE OF INVENTION:  NOVEL G-PROTEIN COUPLED
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  RATNER & PRESTIA
;      STREET:  P.O. BOX 980
;      CITY:  VALLEY FORGE
;      STATE:  PA
;      COUNTRY:  USA
;      ZIP:  19482
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/846,705
;      FILING DATE:  30-APR-1997
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  PRESTIA, PAUL F
;      REGISTRATION NUMBER:  23,031
;      REFERENCE/DOCKET NUMBER:  GH-70003
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-407-0700
;      TELEFAX:  610-407-0701
;      TELEX:  846169
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1170 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-846-705-1

  Query Match             97.2%;  Score 1078.4;  DB 2;  Length 1170;
  Best Local Similarity   99.4%;  Pred. No. 1.4e-247;
  Matches 1082;  Conservative    0;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||||  ||| ||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               |||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              ||||||||||||||||||||||||||||||| |||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
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RESULT 9
PCT-US95-05616-1
; Sequence 1, Application PC/TUS9505616
;  GENERAL INFORMATION:
;    APPLICANT:  LI, ET AL.
;    TITLE OF INVENTION:  Human Neuropeptide Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
;      SOFTWARE:  WORD PERFECT 5.1
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/US95/05616
;      FILING DATE:  concurrently
;      CLASSIFICATION:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  FERRARO, GREGORY D.
;      REGISTRATION NUMBER:  36,134
;      REFERENCE/DOCKET NUMBER:  325800-268
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  201-994-1700
;      TELEFAX:  201-994-1744
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1209 BASE PAIRS
;      TYPE:  NUCLEIC ACID
;      STRANDEDNESS:  SINGLE
;      TOPOLOGY:  LINEAR
;    MOLECULE TYPE:  cDNA
PCT-US95-05616-1
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Query Match 97.1%; Score 1077.8; DB 5; Length 1209;
Best Local Similarity 99.4%; Pred. No. 1.9e-247;
Matches 1082; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCCCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              || ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AACCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGGC 1089
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Db       1081 CTCAGTGGC 1089
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RESULT 10
US-08-462-509B-5
; Sequence 5, Application US/08462509B
; Patent No. 6410701
;  GENERAL INFORMATION:
;    APPLICANT:  Soppet, Daniel et al
;    TITLE OF INVENTION:  Human Neuropeptide Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Human Genome Sciences, Inc.
;      STREET:  9410 Key West Avenue
;      CITY:  Rockiville
;      STATE:  MD
;      COUNTRY:  USA
;      ZIP:  20850
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/462,509B
;      FILING DATE:  05-JUN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  WO PCT/US95/05616
;      FILING DATE:  05-MAY-1995
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Wales, Michele M.
;      REGISTRATION NUMBER:  43,975
;      REFERENCE/DOCKET NUMBER:  PF168P1
;    TELECOMMUNICATION INFORMATION:
```

; TELEPHONE: 301-309-8504
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1116 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1116
US-08-462-509B-5

Query Match 96.9%; Score 1075.2; DB 4; Length 1116;
Best Local Similarity 99.3%; Pred. No. 7.9e-247;
Matches 1080; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
              ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
              ||||||||
Db       1081 CTCAGTGG 1088
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RESULT 11
PCT-US95-05616-5
; Sequence 5, Application PC/TUS9505616
;  GENERAL INFORMATION:
;    APPLICANT:  LI, ET AL.
;    TITLE OF INVENTION:  Human Neuropeptide Receptor
;    NUMBER OF SEQUENCES:  12
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  CARELLA, BYRNE, BAIN, GILFILLAN,
;      ADDRESSEE:  CECCHI, STEWART & OLSTEIN
;      STREET:  6 BECKER FARM ROAD
;      CITY:  ROSELAND
;      STATE:  NEW JERSEY
;      COUNTRY:  USA
;      ZIP:  07068
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  3.5 INCH DISKETTE
;      COMPUTER:  IBM PS/2
;      OPERATING SYSTEM:  MS-DOS
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;       SOFTWARE:  WORD PERFECT 5.1
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US95/05616
;       FILING DATE:  concurrently
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  FERRARO, GREGORY D.
;       REGISTRATION NUMBER:  36,134
;       REFERENCE/DOCKET NUMBER:  325800-268
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  201-994-1700
;       TELEFAX:  201-994-1744
;   INFORMATION FOR SEQ ID NO:  5:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1133 BASE PAIRS
;       TYPE:  NUCLEIC ACID
;       STRANDEDNESS:  SINGLE
;       TOPOLOGY:  LINEAR
;     MOLECULE TYPE:  cDNA
PCT-US95-05616-5

  Query Match             96.9%;  Score 1075.2;  DB 5;  Length 1133;
  Best Local Similarity   99.3%;  Pred. No. 7.9e-247;
  Matches 1080;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              ||||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
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Db       1081 CTCAGTGG 1088
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RESULT 12
US-08-513-974B-375
; Sequence 375, Application US/08513974B
; Patent No. 6114139
; GENERAL INFORMATION:
; APPLICANT: Hinuma, Shuji
; APPLICANT: Hosoya, Masaki
; APPLICANT: Fujii, Ryo
; APPLICANT: Ohtaki, Tetsuya
; APPLICANT: Fukusumi, Shoji
; APPLICANT: Ohgi, Kazuhiro
; TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,

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;     TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;     NUMBER OF SEQUENCES:  380
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;       STREET:  130 Water Street
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02109
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/513,974B
;       FILING DATE:  14-SEP-1995
;       CLASSIFICATION:  536
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/JP95/01599
;       FILING DATE:  10-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-093989
;       FILING DATE:  19-AUG-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-057186
;       FILING DATE:  16-MAR-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 7-007177
;       FILING DATE:  20-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-326611
;       FILING DATE:  28-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-270017
;       FILING DATE:  02-NOV-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236357
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236356
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189274
;       FILING DATE:  11-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189273
;       FILING DATE:  11-AUG-1945
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189272
;       FILING DATE:  11-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Resnick, David S.
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  45753
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
```

; TELEFAX: 617-523-6440
; INFORMATION FOR SEQ ID NO: 375:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 843 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 28..816
US-08-513-974B-375

Query Match 62.0%; Score 688; DB 3; Length 843;
Best Local Similarity 89.2%; Pred. No. 1e-154;
Matches 742; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

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Qy        252 CATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCT 311
              | |  ||| |||||| ||||| || || |||||||| || |||||||||||||||| ||
Db          9 CGTGTTCATCCTGTCACTGGCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCT 68

Qy        312 GCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTA 371
              |||||| |||||||| || |||||||| || ||||||||||||||||||||||||||||
Db         69 GCTGGTAGACATCACGGAATCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTA 128

Qy        372 TCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCG 431
              ||||||||| |||||||||||||||  ||||| |||||||||| |||| ||||||||||
Db        129 TCTACAGGCCGTGTCCGTGTCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCG 188

Qy        432 CTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTC 491
              |||||| |||||||||||||| || |||||||||||||| |||||||| ||||| |||||
Db        189 CTGGTACGCCATCTGCCACCCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTC 248

Qy        492 CATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCA 551
              |||||| |||||||||| |||||||||| |||||||||| |||||||| |||||| |
Db        249 CATCCTCGGCATCTGGGCGGTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGA 308

Qy        552 ATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGA 611
               |  ||||| |||||||| ||||| |||||||||| || ||| | ||  ||||| ||||
Db        309 GTGTAGCAGCGTGCTGCCCGAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGA 368

Qy        612 ACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTA 671
              |||||||||| ||||| || |||||||||||||||| |||||||| ||||||||||
Db        369 GCGCTGGGCAGACGACCTGTACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTA 428

Qy        672 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGG 731
              |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        429 CCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGG 488

Qy        732 CCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCA 791
              |||||||||||||||||||||| || |||||||| |||||||||| ||||||||||
Db        489 CCGCCAGATCCCCGGCACCACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCA 548

Qy        792 GCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCT 851
              |||||  |||| ||  |||||||||||  |||||||||||||||| ||||||||||||
Db        549 GCTGGACGACCAGGGCCAGGGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCT 608
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Qy        852 GGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCT 911
              ||| || ||||| |||||||| || |||||||||| ||||||||||||||||||||||||
Db        609 GGCCGAGGTGAAACAGATGCGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCT 668

Qy        912 GCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTT 971
              |||||||||||||||||||||||| |||||||| |||||||| ||||| |||||||| ||
Db        669 GCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTT 728

Qy        972 CGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCA 1031
              |||||||||||||||||||| ||||| || ||  ||||||||||||||||||||||||||
Db        729 CGGGATGTTCCGCCAAGCCAGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCA 788

Qy       1032 CTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTC 1083
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Db        789 CTGGCTGGTGTACGCCAACAGCGCCGCCAATCCCCTCCTCTACTCCTTCCTC 840
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RESULT 13
US-08-513-974B-55
; Sequence 55, Application US/08513974B
; Patent No. 6114139
;  GENERAL INFORMATION:
;    APPLICANT:  Hinuma, Shuji
;    APPLICANT:  Hosoya, Masaki
;    APPLICANT:  Fujii, Ryo
;    APPLICANT:  Ohtaki, Tetsuya
;    APPLICANT:  Fukusumi, Shoji
;    APPLICANT:  Ohgi, Kazuhiro
;    TITLE OF INVENTION:  G PROTEIN COUPLED RECEPTOR PROTEIN,
;    TITLE OF INVENTION:  PRODUCTION, AND USE THEREOF
;    NUMBER OF SEQUENCES:  380
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
;      STREET:  130 Water Street
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/513,974B
;      FILING DATE:  14-SEP-1995
;      CLASSIFICATION:  536
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  PCT/JP95/01599
;      FILING DATE:  10-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-093989
;      FILING DATE:  19-AUG-1995
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 7-057186
;      FILING DATE:  16-MAR-1995
;    PRIOR APPLICATION DATA:
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;       APPLICATION NUMBER:  JP 7-007177
;       FILING DATE:  20-JAN-1995
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-326611
;       FILING DATE:  28-DEC-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-270017
;       FILING DATE:  02-NOV-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236357
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-236356
;       FILING DATE:  30-SEP-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189274
;       FILING DATE:  11-AUG-1994
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189273
;       FILING DATE:  11-AUG-1945
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP 6-189272
;       FILING DATE:  11-AUG-1994
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Resnick, David S.
;       REGISTRATION NUMBER:  34,235
;       REFERENCE/DOCKET NUMBER:  45753
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-523-3400
;       TELEFAX:  617-523-6440
;   INFORMATION FOR SEQ ID NO:  55:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  789 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-513-974B-55

  Query Match             59.5%;  Score 661;  DB 3;  Length 789;
  Best Local Similarity   89.9%;  Pred. No. 2.6e-148;
  Matches  709;  Conservative    0;  Mismatches   80;  Indels    0;  Gaps    0;

Qy        271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
              || || || |||||||| || |||||||||||||||| |||||||| |||||||| ||
Db          1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy        331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
              |||||||| || |||||||||||||||||||||||||||||||||||||| |||||||||
Db         61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy        391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATGCCATCTGCCAC 450
              |||||||  ||||| |||||||||| |||| |||||||||||||||| ||||||||||||
Db        121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy        451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
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Db        181 CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG 240

Qy        511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCT 570
              ||||||||||| |||||||||| |||||||| |||||| | |  ||||| ||||||||
Db        241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC 300

Qy        571 GAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTC 630
              ||||| |||||||||||  || ||| | ||  ||||| |||| |||||||||| |||||
Db        301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360

Qy        631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
              || ||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
Db        361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCCTC 420

Qy        691 ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
              |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||
Db        421 ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy        751 ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAG 810
              ||||| || |||||||| |||||||||| ||||||||||||||  |||| ||  |||
Db        481 ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy        811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
              ||||||||   |||||||||||||||| |||||||||||||| || ||||| ||||||
Db        541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG 600

Qy        871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 930
              || || |||||||||| ||||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 660

Qy        931 TACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990
              ||||| |||||||| |||||||| ||||| |||||||| ||||||||||||||||||||
Db        661 TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720

Qy        991 AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050
              || ||||| || ||  ||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 780

Qy       1051 AGCGCTGCC 1059
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Db        781 AGCGCCGCC 789


RESULT 14
US-09-461-436B-55
; Sequence 55, Application US/09461436B
; Patent No. 6538107
;   GENERAL INFORMATION:
;        APPLICANT: Shuji Hinuma
;                   Yasuaki Ito
;                   Ryo Fujii
;        TITLE OF INVENTION: G Protein Coupled Receptor Protein,
;                            Production, And Use Thereof
;        NUMBER OF SEQUENCES: 61
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Edwards & Angell, LLP
;             STREET: 101 Federal Street
```

; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02209
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,436B
; FILING DATE: 14-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/513,974
; FILING DATE: 14-SEP-1995
; APPLICATION NUMBER: PCT/JP95/01599
; FILING DATE: 10-AUG-1995
; APPLICATION NUMBER: 7-093989
; FILING DATE: 19-APR-1995
; APPLICATION NUMBER: 7-057186
; FILING DATE: 16-MAR-1995
; APPLICATION NUMBER: 7-007177
; FILING DATE: 20-JAN-1995
; APPLICATION NUMBER: 6-326611
; FILING DATE: 28-DEC-1994
; APPLICATION NUMBER: 6-270017
; FILING DATE: 02-NOV-1994
; APPLICATION NUMBER: 6-236357
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-236356
; FILING DATE: 30-SEP-1994
; APPLICATION NUMBER: 6-189274
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189273
; FILING DATE: 11-AUG-1994
; APPLICATION NUMBER: 6-189272
; FILING DATE: 11-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, DAVID G.
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-09-461-436B-55

Query Match 59.5%; Score 661; DB 4; Length 789;
Best Local Similarity 89.9%; Pred. No. 2.6e-148;

Matches 709; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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Qy        271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
              || || || |||||||| || |||||||||||||||| |||||||| |||||||| ||
Db          1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy        331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
              |||||||| || |||||||||||||||||||||||||||||||||||| |||||||||
Db         61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy        391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATGCCATCTGCCAC 450
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Qy        571 GAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTC 630
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Qy        631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
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Qy        811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
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Qy        991 AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050
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; Sequence 1, Application US/09119788
; Patent No. 6166193
;  GENERAL INFORMATION:
;    APPLICANT:  Yanagisawa, Masashi
;    TITLE OF INVENTION:  CDNA CLONE MY1 THAT ENCODES
;    TITLE OF INVENTION:  A NOVEL HUMAN 7-TRANSMEMBRANE RECEPTOR
;    NUMBER OF SEQUENCES:  2
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SmithKline Beecham Corporation
;      STREET:  709 Swedeland Road
;      CITY:  King of Prussia
;      STATE:  PA
;      COUNTRY:  United States of America
;      ZIP:  19406
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette
;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ for Windows Version 2.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/119,788
;      FILING DATE:  21-JUL-1998
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  60/053,790
;      FILING DATE:  25-JUL-1997
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  King, William T
;      REGISTRATION NUMBER:  30,954
;      REFERENCE/DOCKET NUMBER:  GH50029
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  610-270-5515
;      TELEFAX:  610-270-5090
;      TELEX:
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1633 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  Genomic DNA
US-09-119-788-1

  Query Match           46.1%;  Score 511.8;  DB 3;  Length 1633;
  Best Local Similarity  70.0%;  Pred. No. 1e-112;
  Matches  706;  Conservative    0;  Mismatches  297;  Indels    6;  Gaps    1;

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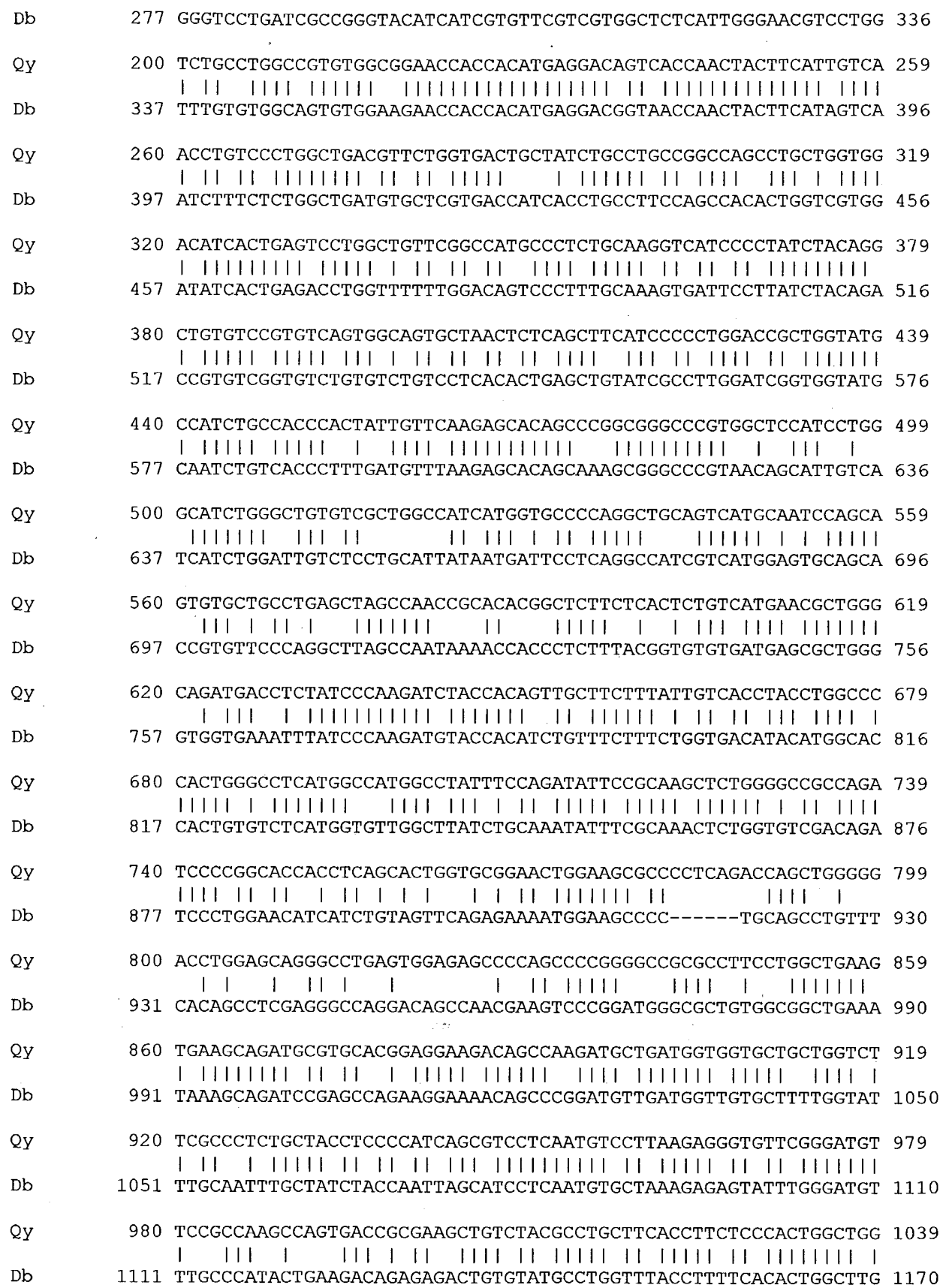

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Search completed: October 15, 2004, 22:55:08
Job time : 90.0094 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: October 15, 2004, 19:59:43 ; Search time 572.496 Seconds
(without alignments)
9829.265 Million cell updates/sec

Title: US-10-070-532-3
Perfect score: 1110
Sequence: 1 atggagccctcagccacccc.....ttccctggagtctgctctaa 1110

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_NA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	% Query

	No.	Score	Match	Length	DB	ID	Description
	1	1110	100.0	1110	10	US-09-393-696-3	Sequence 3, Appli
	2	1102	99.3	1110	14	US-10-077-874-3	Sequence 3, Appli
	3	1079.4	97.2	1564	15	US-10-225-567A-367	Sequence 367, App
	4	1079.4	97.2	1564	16	US-10-352-684A-21	Sequence 21, Appl
	5	1077.8	97.1	1209	10	US-09-393-696-1	Sequence 1, Appli
	6	1077.8	97.1	1209	14	US-10-077-874-1	Sequence 1, Appli
	7	1077.8	97.1	1564	9	US-09-828-538-23	Sequence 23, Appl
	8	1075.2	96.9	1116	14	US-10-077-874-5	Sequence 5, Appli
	9	1075.2	96.9	1133	10	US-09-393-696-5	Sequence 5, Appli
	10	1074.6	96.8	1278	11	US-09-826-509-548	Sequence 548, App
	11	905	81.5	1281	9	US-09-730-931-1	Sequence 1, Appli
	12	661	59.5	789	15	US-10-278-087A-55	Sequence 55, Appl
	13	511.8	46.1	1633	15	US-10-282-717-1	Sequence 1, Appli
	14	511.8	46.1	1843	15	US-10-225-567A-369	Sequence 369, App
	15	507	45.7	1335	11	US-09-826-509-550	Sequence 550, App
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	17	241.2	21.7	10453	9	US-09-828-538-21	Sequence 21, Appl
	18	236	21.3	244	9	US-09-828-538-6	Sequence 6, Appli
	19	223.8	20.2	227	9	US-09-828-538-10	Sequence 10, Appl
	20	199	17.9	356	9	US-09-828-538-2	Sequence 2, Appli
	21	179	16.1	179	9	US-09-828-538-4	Sequence 4, Appli
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	26	161.6	14.6	1320	9	US-09-292-973-3	Sequence 3, Appli
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	33	119	10.7	1174	17	US-10-611-210-9	Sequence 9, Appli
	34	117.4	10.6	1110	14	US-10-044-592-17	Sequence 17, Appl
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	36	117.4	10.6	1113	15	US-10-225-567A-244	Sequence 244, App
	37	117.4	10.6	1152	17	US-10-611-210-10	Sequence 10, Appl
	38	117.4	10.6	1174	17	US-10-611-210-7	Sequence 7, Appli
	39	117.4	10.6	1331	14	US-10-044-592-73	Sequence 73, Appl
	40	116.8	10.5	1173	17	US-10-611-210-6	Sequence 6, Appli
	41	116	10.5	116	9	US-09-828-538-8	Sequence 8, Appli
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c	45	104	9.4	436	16	US-10-027-632-275272	Sequence 275272,

ALIGNMENTS

RESULT 1
US-09-393-696-3
; Sequence 3, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:

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;  APPLICANT: Human Genome Sciences, Inc. et al.
;  TITLE OF INVENTION: Human Neuropeptide Receptor
;  FILE REFERENCE: PF168P2
;  CURRENT APPLICATION NUMBER: US/09/393,696
;  CURRENT FILING DATE: 1999-09-10
;  EARLIER APPLICATION NUMBER: PCT/US95/05616
;  EARLIER FILING DATE: 1995-05-05
;  EARLIER APPLICATION NUMBER: US08/462,509
;  EARLIER FILING DATE: 1995-06-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
;   LENGTH: 1110
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1110)
US-09-393-696-3

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  Best Local Similarity   100.0%;  Pred. No. 9.1e-303;
  Matches 1110;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 2
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; Sequence 3, Application US/10077874
; Publication No. US20020115155A1
; GENERAL INFORMATION:
; APPLICANT: Soppet, Daniel et al
; TITLE OF INVENTION: Human Neuropeptide Receptor
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: MD

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;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/077,874
;             FILING DATE: 20-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/462,509
;             FILING DATE: 05-JUNE-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wales, Michele M.
;             REGISTRATION NUMBER: 43,975
;             REFERENCE/DOCKET NUMBER: PF168P1D1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 301-309-8504
;             TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1110 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
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US-10-077-874-3

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  Best Local Similarity   99.5%;  Pred. No. 1.6e-300;
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Db       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
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Db       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy       541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Db       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy       601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
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Db       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
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Db       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
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Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
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Db       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db      1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

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RESULT 3
US-10-225-567A-367
; Sequence 367, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 367
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-367

Query Match 97.2%; Score 1079.4; DB 15; Length 1564;
Best Local Similarity 99.4%; Pred. No. 4.2e-294;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db        274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573
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; APPLICANT: Weich, Nadine S.
; APPLICANT: Kelly, Louise M.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: HEMATOLOGICAL DISORDERS USING 131, 148, 199, 12303,
13906,
; TITLE OF INVENTION: 15513, 17822, 302, 5677, 194, 14393, 28059, 7366, 12212,
; TITLE OF INVENTION: 1981, 261, 12416, 270, 1410, 137, 1871, 13051, 1847,
1849,
; TITLE OF INVENTION: 15402, 340, 10217, 837, 1761, 8990 OR 13249 MOLECULES
; FILE REFERENCE: MPI02-019P1RNOMNIM
; CURRENT APPLICATION NUMBER: US/10/352,684A
; CURRENT FILING DATE: 2003-01-28
; PRIOR APPLICATION NUMBER: US 60/354,333
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: US 60/360,258
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/364,476
; PRIOR FILING DATE: 2002-03-15
; PRIOR APPLICATION NUMBER: US 60/375,626
; PRIOR FILING DATE: 2002-04-26
; PRIOR APPLICATION NUMBER: US 60/386,494
; PRIOR FILING DATE: 2002-06-06
; PRIOR APPLICATION NUMBER: US 60/390,965
; PRIOR FILING DATE: 2002-06-24
; PRIOR APPLICATION NUMBER: US 60/392,480
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: US 60/394,128
; PRIOR FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/399,783
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: US 60/403,221
; PRIOR FILING DATE: 2002-08-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 1564
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (154)...(1431)
US-10-352-684A-21

Query Match 97.2%; Score 1079.4; DB 16; Length 1564;
Best Local Similarity 99.4%; Pred. No. 4.2e-294;
Matches 1083; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

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Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 273

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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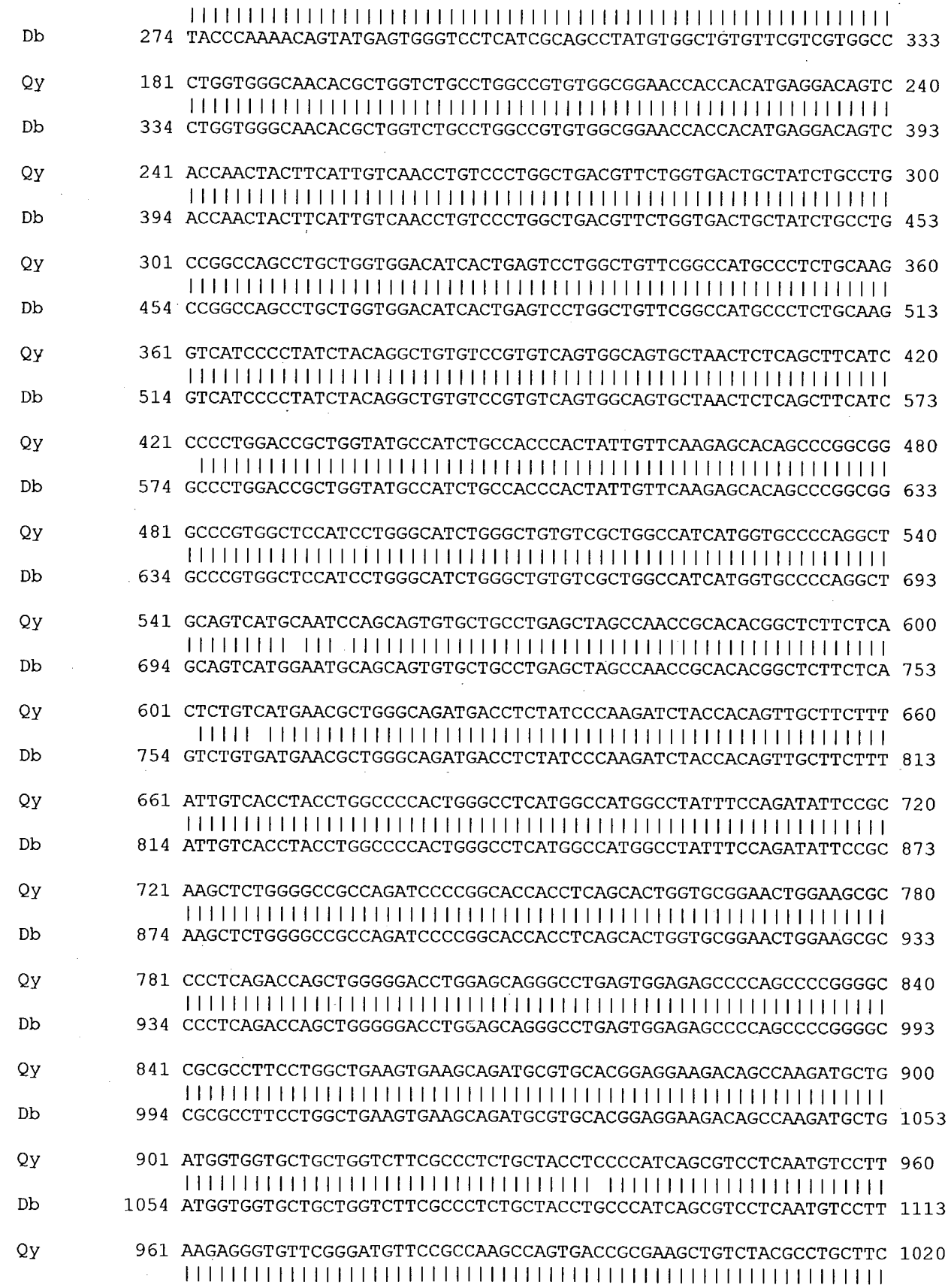
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Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
Db 454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513
Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573
Qy 421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633
Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693
Qy 541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
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Qy 601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813
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Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933
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Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113
Qy 961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

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Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

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Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
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Db       1234 CTCAGTGGC 1242


RESULT 5
US-09-393-696-1
; Sequence 1, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc. et al.
;  TITLE OF INVENTION: Human Neuropeptide Receptor
;  FILE REFERENCE: PF168P2
;  CURRENT APPLICATION NUMBER: US/09/393,696
;  CURRENT FILING DATE: 1999-09-10
;  EARLIER APPLICATION NUMBER: PCT/US95/05616
;  EARLIER FILING DATE: 1995-05-05
;  EARLIER APPLICATION NUMBER: US08/462,509
;  EARLIER FILING DATE: 1995-06-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 1209
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1209)
US-09-393-696-1

  Query Match             97.1%;  Score 1077.8;  DB 10;  Length 1209;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-293;
  Matches 1082;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

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                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
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Db        1081 CTCAGTGGC 1089


RESULT 6
US-10-077-874-1
; Sequence 1, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;        APPLICANT: Soppet, Daniel et al
;        TITLE OF INVENTION: Human Neuropeptide Receptor
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: MD
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/077,874
;             FILING DATE: 20-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/462,509
;             FILING DATE: 05-JUNE-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wales, Michele M.
;             REGISTRATION NUMBER: 43,975
;             REFERENCE/DOCKET NUMBER: PF168P1D1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 301-309-8504
;             TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1209 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1209
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-077-874-1

  Query Match             97.1%;  Score 1077.8;  DB 14;  Length 1209;
  Best Local Similarity   99.4%;  Pred. No. 1.1e-293;
  Matches 1082;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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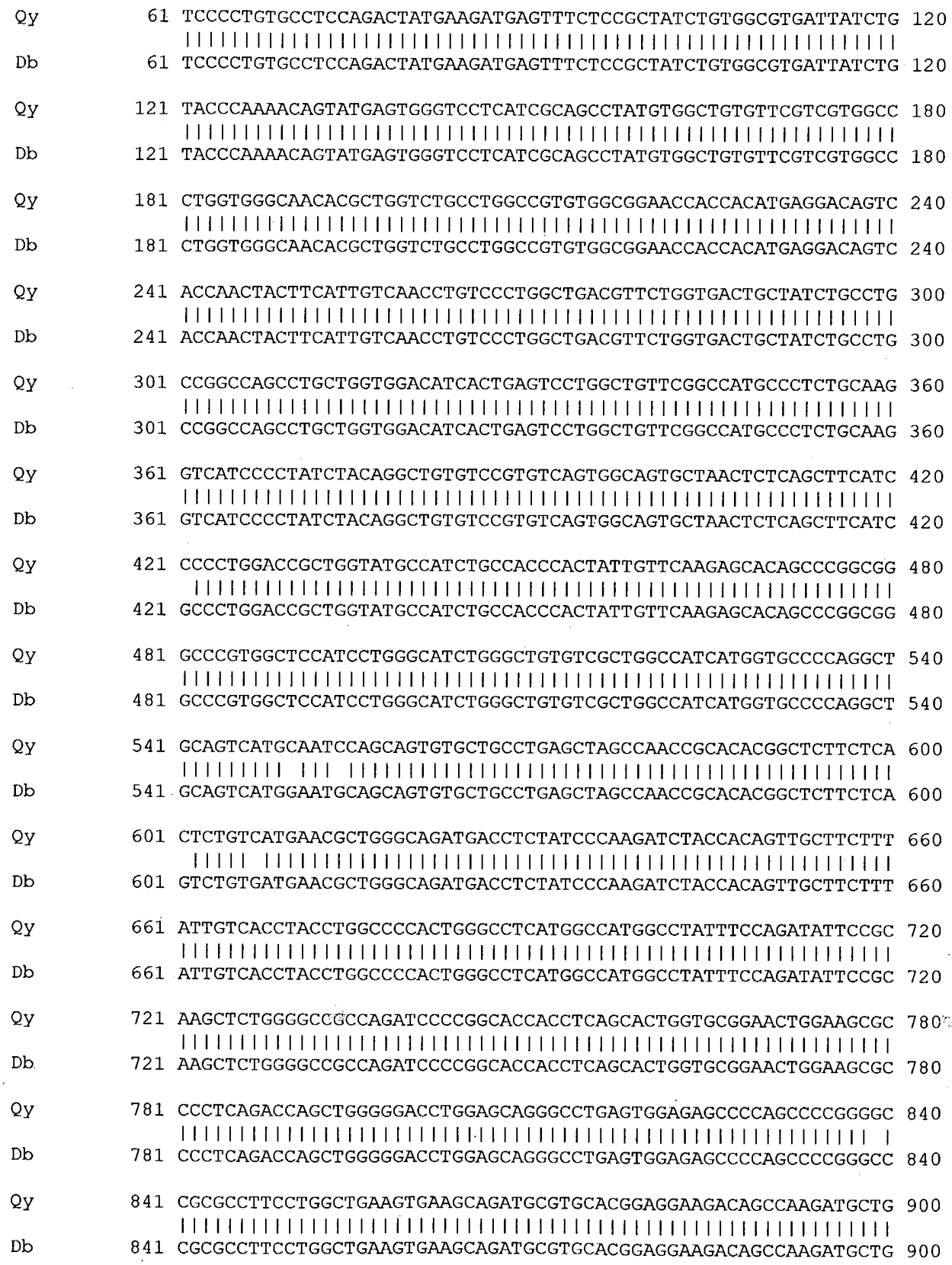

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RESULT 7
US-09-828-538-23
; Sequence 23, Application US/09828538
; Patent No. US20010025031A1
; GENERAL INFORMATION:
;  APPLICANT: Ellis, Catherine E.
;  APPLICANT:  Kwok, Cheni
;  APPLICANT:  Bodsworth, Nicola J.
;  APPLICANT:  Halsey, Wendy
;  APPLICANT:  Van Horn, Stephanie
;  TITLE OF INVENTION: HFGAN72 Receptor Genomic DNA and Methods
;  TITLE OF INVENTION:  of Use Thereof in Diagnostic Applications
;  FILE REFERENCE: GH-50038-C1
;  CURRENT APPLICATION NUMBER: US/09/828,538
;  CURRENT FILING DATE:  2001-04-06
;  PRIOR APPLICATION NUMBER: 60/088,624
;  PRIOR FILING DATE: 1998-06-08
;  PRIOR APPLICATION NUMBER: 60/093,726
;  PRIOR FILING DATE: 1998-07-22
;  PRIOR APPLICATION NUMBER: 09/328,014
;  PRIOR FILING DATE: 1999-06-08
;  NUMBER OF SEQ ID NOS: 24
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 23
;   LENGTH: 1564
;   TYPE: DNA
;   ORGANISM: HOMO SAPIENS
US-09-828-538-23
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  Query Match             97.1%;  Score 1077.8;  DB 9;  Length 1564;
  Best Local Similarity   99.4%;  Pred. No. 1.2e-293;
  Matches 1082;  Conservative    0;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        154 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 213

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              |||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        214 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGCGATTATCTG 273
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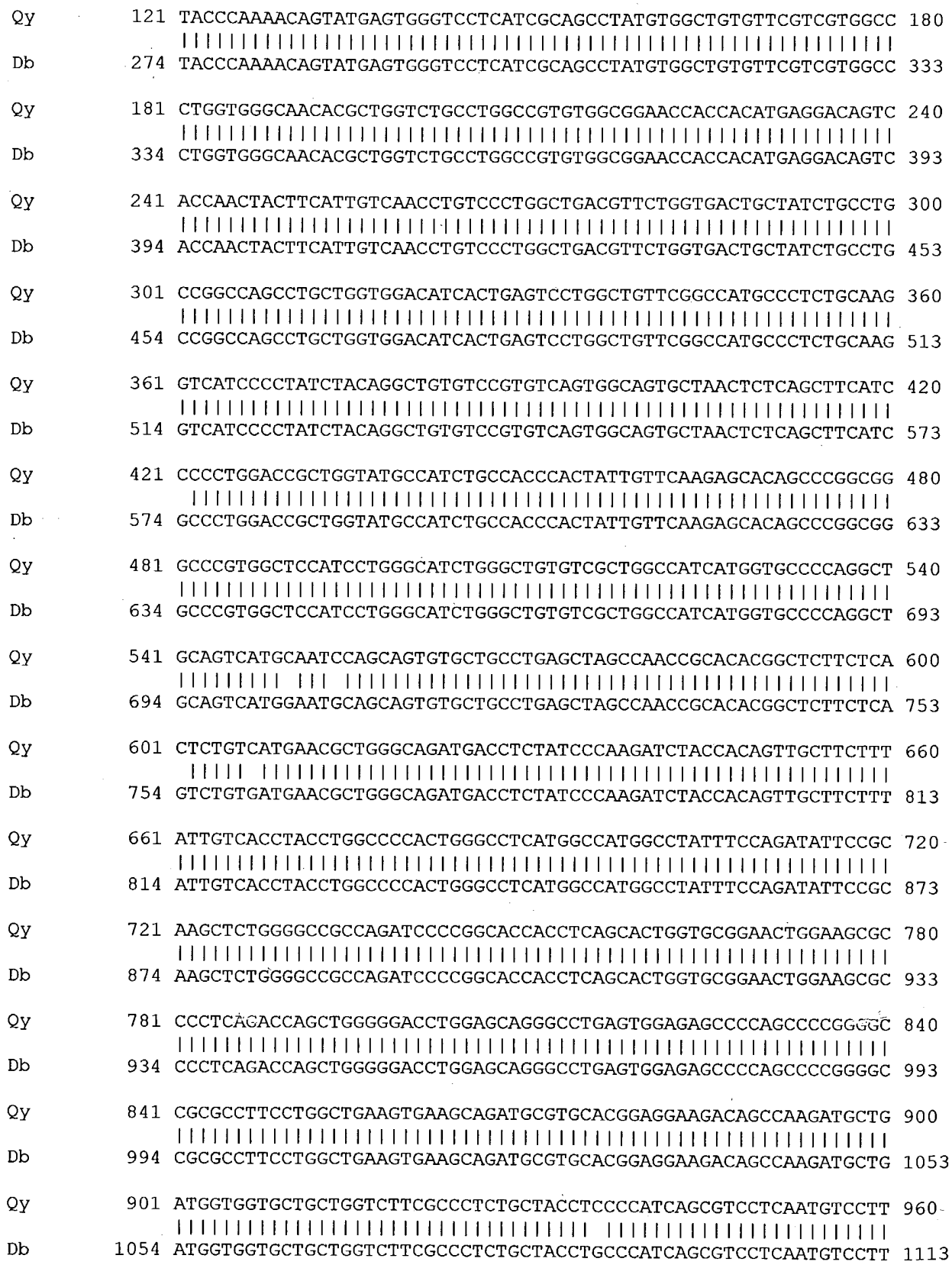
Qy 121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
Db 274 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 333
Qy 181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
Db 334 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 393
Qy 241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
Db 394 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 453
Qy 301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
Db 454 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 513
Qy 361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
Db 514 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 573
Qy 421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
Db 574 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 633
Qy 481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
Db 634 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 693
Qy 541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
Db 694 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 753
Qy 601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
Db 754 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 813
Qy 661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
Db 814 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 873
Qy 721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
Db 874 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 933
Qy 781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
Db 934 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 993
Qy 841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
Db 994 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 1053
Qy 901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
Db 1054 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 1113

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Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1114 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1173

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1174 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1233

Qy       1081 CTCAGTGGC 1089
              |||||||||
Db       1234 CTCAGTGGC 1242


RESULT 8
US-10-077-874-5
; Sequence 5, Application US/10077874
; Publication No. US20020115155A1
;   GENERAL INFORMATION:
;        APPLICANT: Soppet, Daniel et al
;        TITLE OF INVENTION: Human Neuropeptide Receptor
;        NUMBER OF SEQUENCES: 12
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Human Genome Sciences, Inc.
;             STREET: 9410 Key West Avenue
;             CITY: Rockville
;             STATE: MD
;             COUNTRY: USA
;             ZIP: 20850
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/077,874
;             FILING DATE: 20-Feb-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/462,509
;             FILING DATE: 05-JUNE-1995
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Wales, Michele M.
;             REGISTRATION NUMBER: 43,975
;             REFERENCE/DOCKET NUMBER: PF168P1D1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 301-309-8504
;             TELEFAX: 301-309-8439
;   INFORMATION FOR SEQ ID NO: 5:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1116 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: DNA (genomic)
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  1..1116
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; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-077-874-5

Query Match 96.9%; Score 1075.2; DB 14; Length 1116;
Best Local Similarity 99.3%; Pred. No. 5.9e-293;
Matches 1080; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGACCCC 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120

Qy        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy        421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy        541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
              |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy        601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
               ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
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Db        721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900

Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
              |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
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Db       1081 CTCAGTGG 1088
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RESULT 9
US-09-393-696-5
; Sequence 5, Application US/09393696
; Publication No. US20030022277A1
; GENERAL INFORMATION:
;  APPLICANT: Human Genome Sciences, Inc. et al.
;  TITLE OF INVENTION: Human Neuropeptide Receptor
;  FILE REFERENCE: PF168P2
;  CURRENT APPLICATION NUMBER: US/09/393,696
;  CURRENT FILING DATE: 1999-09-10
;  EARLIER APPLICATION NUMBER: PCT/US95/05616
;  EARLIER FILING DATE: 1995-05-05
;  EARLIER APPLICATION NUMBER: US08/462,509
;  EARLIER FILING DATE: 1995-06-05
;  NUMBER OF SEQ ID NOS: 23
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
;   LENGTH: 1133
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(1131)
US-09-393-696-5

  Query Match            96.9%;  Score 1075.2;  DB 10;  Length 1133;
  Best Local Similarity  99.3%;  Pred. No. 6e-293;
  Matches 1080;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60
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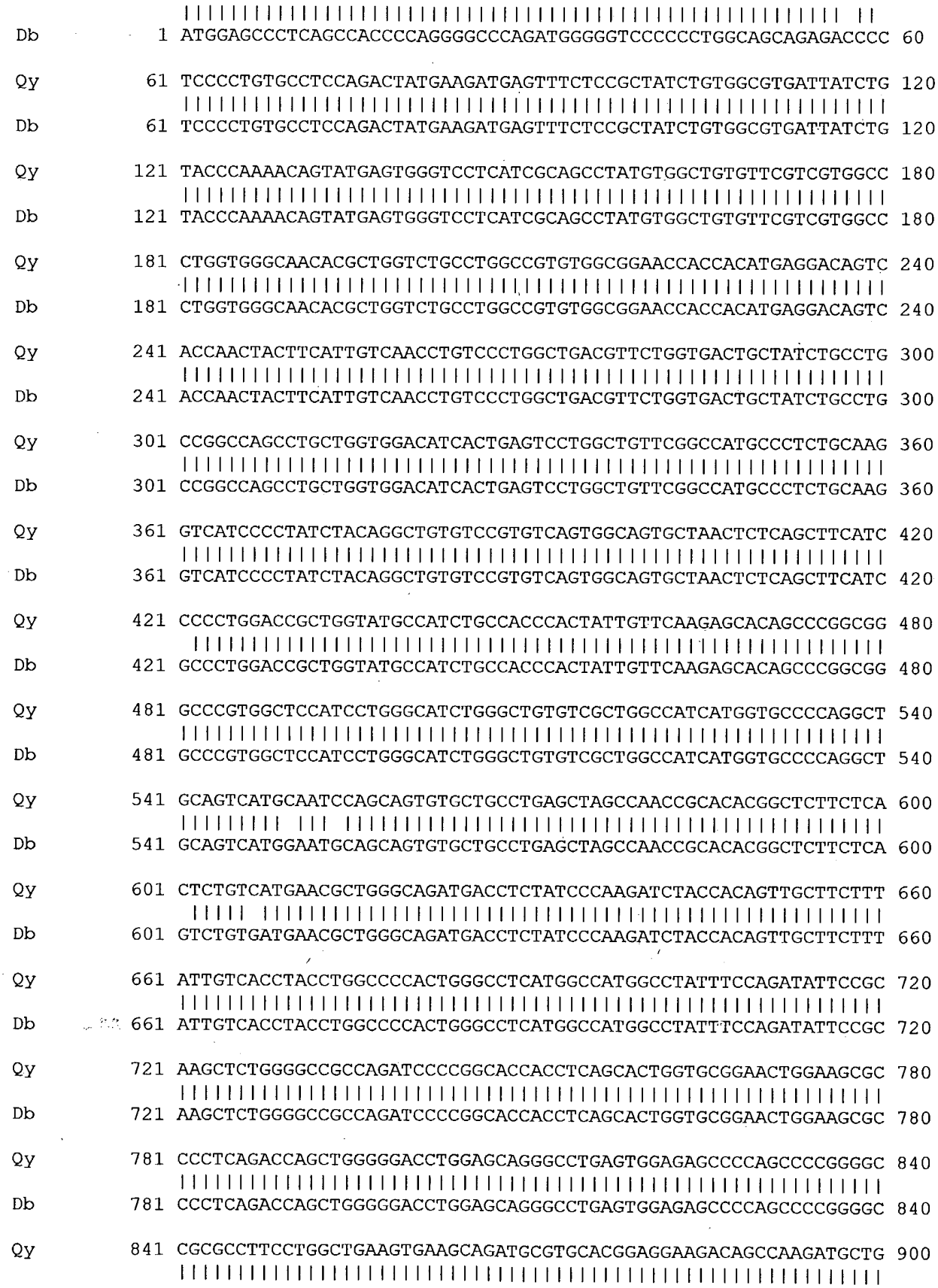

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Qy        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
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Db        901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
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Db       1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy       1081 CTCAGTGG 1088
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RESULT 10
US-09-826-509-548
; Sequence 548, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 548
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-548

Query Match 96.8%; Score 1074.6; DB 11; Length 1278;
Best Local Similarity 99.2%; Pred. No. 9e-293;
Matches 1080; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

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Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGATGGGGGTCCCCCCTGGCAGCAGAGAGCCG 60

Qy         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 TCCCCTGTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTG 120
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Qy       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180
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Db       121 TACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCC 180

Qy       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       181 CTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTC 240

Qy       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       241 ACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTG 300

Qy       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       301 CCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAG 360

Qy       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       361 GTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATC 420

Qy       421 CCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       421 GCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGG 480

Qy       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       481 GCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCT 540

Qy       541 GCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600
            |||||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db       541 GCAGTCATGGAATGCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCA 600

Qy       601 CTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660
             ||||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       601 GTCTGTGATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTT 660

Qy       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       661 ATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGC 720

Qy       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       721 AAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGC 780

Qy       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840
            ||||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db       781 CCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGC 840

Qy       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTG 900
            ||||||||||||||||||||||||||||||||||||||||||||||||||   |||||||||
Db       841 CGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAAAAAAGATGCTG 900

Qy       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTT 960
            |||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db       901 ATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTGCCCATCAGCGTCCTCAATGTCCTT 960

Qy       961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020
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Db         961 AAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTC 1020

Qy        1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080
                 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        1021 ACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTC 1080

Qy        1081 CTCAGTGGC 1089
                 |||||||||
Db        1081 CTCAGTGGC 1089


RESULT 11
US-09-730-931-1
; Sequence 1, Application US/09730931
; Patent No. US20020064814A1
; GENERAL INFORMATION:
;  APPLICANT:  ELLIS, CATHERINE E.
;  TITLE OF INVENTION:  DOG OREXIN 1 RECEPTOR
;  FILE REFERENCE:  GH-70669
;  CURRENT APPLICATION NUMBER: US/09/730,931
;  CURRENT FILING DATE:  2000-12-06
;  PRIOR APPLICATION NUMBER:  60/169,373
;  PRIOR FILING DATE:  1999-12-07
;  NUMBER OF SEQ ID NOS:  2
;  SOFTWARE:  FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 1281
;   TYPE: DNA
;   ORGANISM: CANIS FAMILIARIS
US-09-730-931-1

  Query Match             81.5%;  Score 905;  DB 9;  Length 1281;
  Best Local Similarity   89.9%;  Pred. No. 6.2e-245;
  Matches  984;  Conservative    0;  Mismatches  105;  Indels    6;  Gaps    1;

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              |||||||||||||||||||||||||||||||  |||  |||| | ||| || | |||| |
Db          1 ATGGAGCCCTCAGCCACCCCAGGGGCCCAGACTGGGACCCCCACCGGCGGCGGGGAGCTG 60

Qy         61 TCCCCT------GTGCCTCCAGACTATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGAT 114
              || ||       |||||||| |||||||||| ||||| || |||||||||||||| |||
Db         61 TCTCCGTCACTGGTGCCTCCCGACTATGAAGACGAGTTCCTGCGCTATCTGTGGCGCGAT 120

Qy        115 TATCTGTACCCAAAACAGTATGAGTGGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTC 174
              || |||||||||| |||||||||||||||||||| ||||| |||||||||||| |
Db        121 TACCTGTACCCAAAGCAGTATGAGTGGGTCCTCATCGCTGCCTACGTGGCTGTGTTCCTA 180

Qy        175 GTGGCCCTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGCGGAACCACCACATGAGG 234
              |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||
Db        181 GTGGCCCTGGTGGGCAACACGCTGGTCTGCCTGGCCGTGTGGAGGAACCACCACATGAGG 240

Qy        235 ACAGTCACCAACTACTTCATTGTCAACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATC 294
              || |||||||||| |||||||||||||||||||||||| || |||||||| || |||
Db        241 ACGGTCACCAACTATTTCATTGTCAACCTGTCCCTGGCTGATGTGCTGGTGACAGCCATC 300

Qy        295 TGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTC 354
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                 ||||| |||||||||||||||| |||||||||||||||||||| ||||| ||| |||||
Db        301 TGCCTCCCGGCCAGCCTGCTGGTAGACATCACTGAGTCCTGGCTCTTCGGTCATACCCTC 360

Qy        355 TGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGC 414
                 ||||| |||||||||||| |||||||| ||||| ||||| |||||||||||| |||||||||
Db        361 TGCAAAGTCATCCCCTACCTACAGGCCGTGTCTGTGTCGGTGGCAGTGCTGACTCTCAGC 420

Qy        415 TTCATCCCCCTGGACCGCTGGTATGCCATCTGCCACCCACTATTGTTCAAGAGCACAGCC 474
                 |||||| |||||||||||||||||||||||||||||| || |||||||||||||| |||
Db        421 TTCATCGCCCTGGACCGCTGGTATGCCATCTGCCACCCGCTGTTGTTCAAGAGCACCGCC 480

Qy        475 CGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCC 534
                 ||||| |||||  |||||||||||||||||||||||||||| ||||  ||||||| ||
Db        481 CGGCGCGCCCGCAGCTCCATCCTGGGCATCTGGGCTGTGTCATTGGCTGTCATGGTACCT 540

Qy        535 CAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTC 594
                 |||||||| |||||| ||| |||||| ||||| |||||||||||||||||| || |||
Db        541 CAGGCTGCCGTCATGGAATGCAGCAGCGTGCTCCCTGAGCTAGCCAACCGCACCCGCCTC 600

Qy        595 TTCTCACTCTGTCATGAACGCTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGC 654
                 |||||  | ||| |||||| ||||||||||||||||||||||||||||||||||||||||
Db        601 TTCTCTGTGTGTGATGAACACTGGGCAGATGACCTCTATCCCAAGATCTACCACAGTTGC 660

Qy        655 TTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATA 714
                 ||||| |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        661 TTCTTCATTGTCACCTACTTGGCCCCACTGGGCCTCATGGCCATGGCCTATTTCCAGATC 720

Qy        715 TTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACCACCTCAGCACTGGTGCGGAACTGG 774
                 |||||||||||||||||||||||||||||| |||||||| || || |||||| ||||||||
Db        721 TTCCGCAAGCTCTGGGGCCGCCAGATCCCTGGCACCACATCGGCCCTGGTGAGGAACTGG 780

Qy        775 AAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCC 834
                 ||||| ||||| |||||||||| ||||| || ||  |||||||| |  || ||||  ||
Db        781 AAGCGGCCCTCGGACCAGCTGGAGGACCAGGGGCCCGGCCTGAGCGCGGAACCCCCCCCT 840

Qy        835 CGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAG 894
                 |||| ||| |||||||||||||| |||||||||||||| || |||||||||| ||||||
Db        841 CGGGCCCGGGCCTTCCTGGCTGAGGTGAAGCAGATGCGAGCGCGGAGGAAGACGGCCAAG 900

Qy        895 ATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAAT 954
                 |||||||||||| |||||||||||| |||||||||||||| |||||||| |||||||||
Db        901 ATGCTGATGGTGCTGCTGCTGGTCTTTGCCCTCTGCTACCTGCCCATCAGTGTCCTCAAT 960

Qy        955 GTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCC 1014
                 ||||| |||||||||||||||||||||||||| |||||||||| ||||| || ||||||
Db        961 GTCCTCAAGAGGGTGTTCGGGATGTTCCGCCAATCCAGTGACCGAGAAGCCGTGTACGCC 1020

Qy       1015 TGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAACAGCGCTGCCAACCCCATCATCTAC 1074
                 |||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db       1021 TGCTTCACCTTCTCCCACTGGCTGGTGTATGCCAACAGCGCTGCCAACCCCATCATCTAC 1080

Qy       1075 AACTTCCTCAGTGGC 1089
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Db       1081 AACTTCCTCAGCGGC 1095
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RESULT 12

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US-10-278-087A-55
; Sequence 55, Application US/10278087A
; Publication No. US20030138817A1
;   GENERAL INFORMATION:
;        APPLICANT: Shuji Hinuma
;                   Yasuaki Ito
;                   Ryo Fujii
;        TITLE OF INVENTION: G Protein Coupled Receptor Protein,
;                            Production, And Use Thereof
;        NUMBER OF SEQUENCES: 61
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Edwards & Angell, LLP
;             STREET: 101 Federal Street
;             CITY: BOSTON
;             STATE: MA
;             COUNTRY: USA
;             ZIP: 02209
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/278,087A
;             FILING DATE: 31-Jan-2003
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/461,436
;             FILING DATE: 14-DEC-1999
;             APPLICATION NUMBER: 09/038,572
;             FILING DATE: 11-MAR-1998
;             APPLICATION NUMBER: 08/513,974
;             FILING DATE: 14-SEP-1995
;             APPLICATION NUMBER: PCT/JP95/01599
;             FILING DATE: 10-AUG-1995
;             APPLICATION NUMBER: 7-093989
;             FILING DATE: 19-APR-1995
;             APPLICATION NUMBER: 7-057186
;             FILING DATE: 16-MAR-1995
;             APPLICATION NUMBER: 7-007177
;             FILING DATE: 20-JAN-1995
;             APPLICATION NUMBER: 6-326611
;             FILING DATE: 28-DEC-1994
;             APPLICATION NUMBER: 6-270017
;             FILING DATE: 02-NOV-1994
;             APPLICATION NUMBER: 6-236357
;             FILING DATE: 30-SEP-1994
;             APPLICATION NUMBER: 6-236356
;             FILING DATE: 30-SEP-1994
;             APPLICATION NUMBER: 6-189274
;             FILING DATE: 11-AUG-1994
;             APPLICATION NUMBER: 6-189273
;             FILING DATE: 11-AUG-1994
;             APPLICATION NUMBER: 6-189272
;             FILING DATE: 11-AUG-1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: CONLIN, DAVID G.
```

; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 45753 DIV3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-439-4444
; TELEFAX: 617-439-4170
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 789 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 55:
US-10-278-087A-55

Query Match 59.5%; Score 661; DB 15; Length 789;
Best Local Similarity 89.9%; Pred. No. 3.6e-176;
Matches 709; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

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Qy        271 GCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGGACATCACTGAG 330
              || || || |||||||| || |||||||||||||||| |||||||| |||||||| ||
Db          1 GCCGATGTGCTGGTGACAGCCATCTGCCTGCCGGCCAGTCTGCTGGTAGACATCACGGAA 60

Qy        331 TCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCTGTGTCCGTG 390
              |||||||| || |||||||||||||||||||||||||||||||||||| |||||||||
Db         61 TCCTGGCTCTTTGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGGCCGTGTCCGTG 120

Qy        391 TCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATGCCATCTGCCAC 450
              ||||||| ||||| |||||||||| |||| |||||||||||||| ||||||||||||
Db        121 TCAGTGGTCGTGCTGACTCTCAGCTCCATCGCCCTGGACCGCTGGTACGCCATCTGCCAC 180

Qy        451 CCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGGGCATCTGGGCT 510
              || || |||||||||||||| |||||||| ||||| |||||||||| ||||||||||||
Db        181 CCGCTGTTGTTCAAGAGCACTGCCCGGCGCGCCCGCGGCTCCATCCTCGGCATCTGGGCG 240

Qy        511 GTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCAGTGTGCTGCCT 570
              |||||||||||  |||||||||| |||||||| |||||| | |  ||||| ||||||||
Db        241 GTGTCGCTGGCTGTCATGGTGCCTCAGGCTGCTGTCATGGAGTGTAGCAGCGTGCTGCCC 300

Qy        571 GAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGGCAGATGACCTC 630
              ||||| |||||||||||| || ||| | ||  ||||| |||| |||||||||||| |||||
Db        301 GAGCTGGCCAACCGCACCCGCCTCCTGTCTGTCTGTGATGAGCGCTGGGCAGACGACCTG 360

Qy        631 TATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCCCACTGGGCCTC 690
              || |||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
Db        361 TACCCCAAGATCTACCACAGCTGCTTCTTCATTGTCACCTACCTGGCCCCACTGGGCCTC 420

Qy        691 ATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 750
              |||||||||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db        421 ATGGCCATGGCCTATTTCCAGATCTTCCGCAAGCTCTGGGGCCGCCAGATCCCCGGCACC 480

Qy        751 ACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGGACCTGGAGCAG 810
              ||||| || |||||||| |||||||||| |||||||||||||||  |||| ||  |||
Db        481 ACCTCGGCCCTGGTGCGCAACTGGAAGCGGCCCTCAGACCAGCTGGACGACCAGGGCCAG 540

Qy        811 GGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAGTGAAGCAGATG 870
              ||||||||   |||||||||||||||| |||||||||||||| || ||||| |||||||
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Db        541 GGCCTGAGCTCAGAGCCCCAGCCCCGGGCCCGCGCCTTCCTGGCCGAGGTGAAACAGATG 600

Qy        871 CGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 930
              || || |||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        601 CGAGCCCGGAGGAAGACGGCCAAGATGCTGATGGTGGTGCTGCTGGTCTTCGCCCTCTGC 660

Qy        931 TACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGTTCCGCCAAGCC 990
              ||||| |||||||| |||||||| ||||| |||||||| ||||||||||||||||||||
Db        661 TACCTGCCCATCAGTGTCCTCAACGTCCTCAAGAGGGTCTTCGGGATGTTCCGCCAAGCC 720

Qy        991 AGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 1050
              || ||||| || ||  ||||||||||||||||||||||||||||||||||||||||||||
Db        721 AGCGACCGAGAGGCCATCTACGCCTGCTTCACCTTCTCCCACTGGCTGGTGTACGCCAAC 780

Qy       1051 AGCGCTGCC 1059
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Db        781 AGCGCCGCC 789
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RESULT 13
US-10-282-717-1
; Sequence 1, Application US/10282717
; Publication No. US20030083466A1
; GENERAL INFORMATION:
; APPLICANT: YANAGISAWA, MASASHI
; TITLE OF INVENTION: cDNA CLONE MY1 THAT ENCODES A NOVEL
; TITLE OF INVENTION: HUMAN 7-TRANSMEMBRANE RECEPTOR
; FILE REFERENCE: GH50029D1C1
; CURRENT APPLICATION NUMBER: US/10/282,717
; CURRENT FILING DATE: 2002-10-28
; PRIOR APPLICATION NUMBER: 09/676,625
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: 09/119,788
; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: 60/053,790
; PRIOR FILING DATE: 1997-07-25
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1633
; TYPE: DNA
; ORGANISM: HOMO SAPIENS
US-10-282-717-1

Query Match 46.1%; Score 511.8; DB 15; Length 1633;
Best Local Similarity 70.0%; Pred. No. 5.2e-134;
Matches 706; Conservative 0; Mismatches 297; Indels 6; Gaps 1;

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Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
              | || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db        217 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 276

Qy        140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
              ||||||| ||||| |  ||  |    |||||||||||||| ||  | || |||   ||||
Db        277 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 336

Qy        200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
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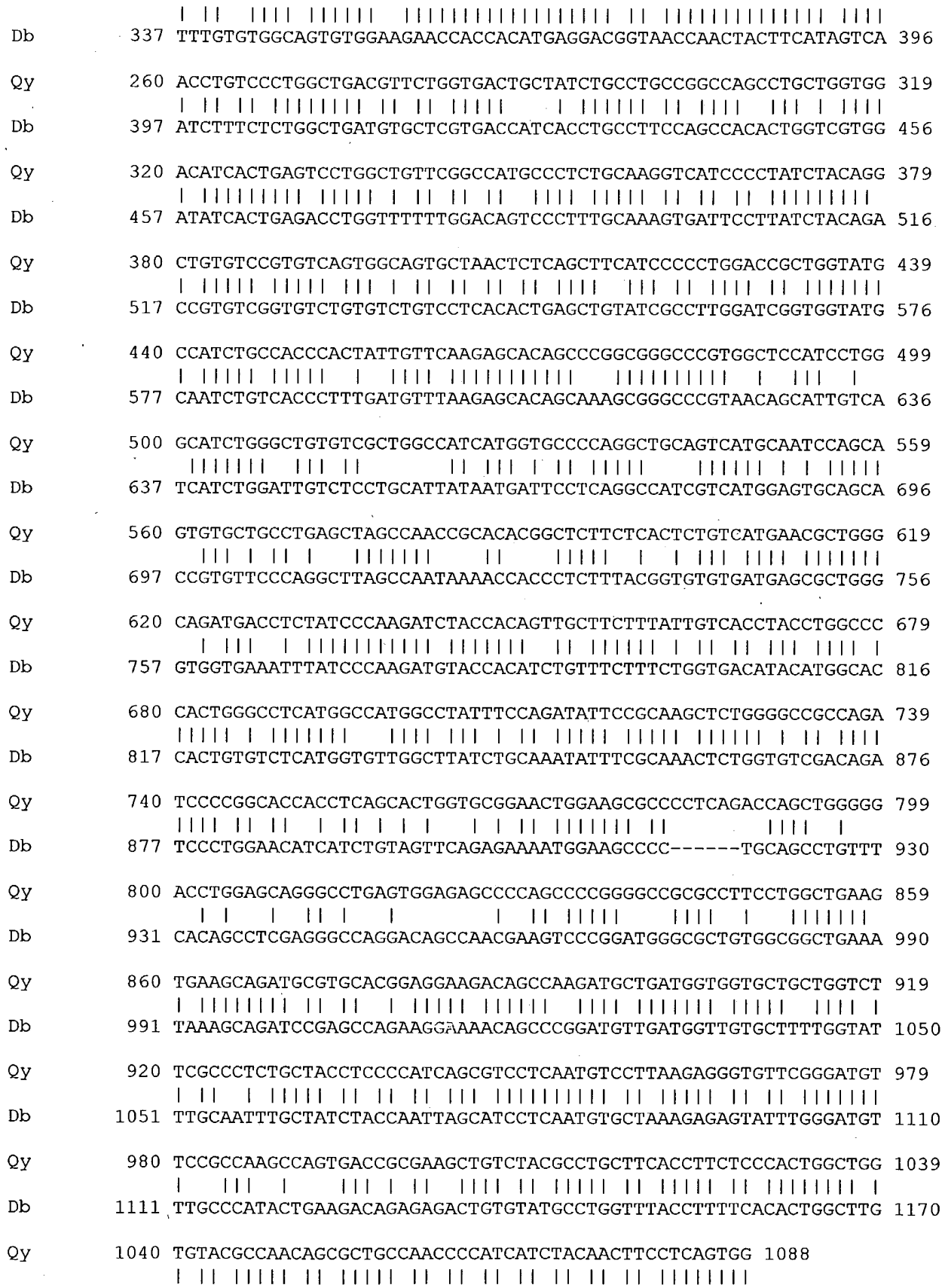

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Db       1171 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGG 1219
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RESULT 14
US-10-225-567A-369
; Sequence 369, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: LifeSpan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burmer, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS (GPCRS)
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 369
; LENGTH: 1843
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-225-567A-369

Query Match 46.1%; Score 511.8; DB 15; Length 1843;
Best Local Similarity 70.0%; Pred. No. 5.3e-134;
Matches 706; Conservative 0; Mismatches 297; Indels 6; Gaps 1;

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Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
              | || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db        428 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 487

Qy        140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
              ||||||| ||||| |  ||  |    |||||||||||||| ||  | || |||   ||||
Db        488 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 547

Qy        200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
              | ||  |||| |||||| ||||||||||||||||| || |||||||||||||| ||||
Db        548 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 607

Qy        260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
              | || || |||||||| || || |||||    | |||||| || ||||  ||| | ||||
Db        608 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 667

Qy        320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
              | ||||||||| ||||| | || || ||  |||| ||||| || || || |||||||||
Db        668 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 727

Qy        380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
              | ||||| ||||| ||| | || || || || |||| ||| || |||| || |||||||
Db        728 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 787

Qy        440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
              | ||||| |||||  |  |||| ||||||||||   |||||||||  |  |||  |
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Db        788 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 847

Qy        500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559

Db        848 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 907

Qy        560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619

Db        908 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 967

Qy        620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679

Db        968 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 1027

Qy        680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739

Db       1028 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 1087

Qy        740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799

Db       1088 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 1141

Qy        800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859

Db       1142 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA 1201

Qy        860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919

Db       1202 TAAAGCAGATCCGAGCCAGAAGGAAAACAGCCCGGATGTTGATGGTTGTGCTTTTGGTAT 1261

Qy        920 TCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979

Db       1262 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 1321

Qy        980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039

Db       1322 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1381

Qy       1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088

Db       1382 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGG 1430
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RESULT 15
US-09-826-509-550
; Sequence 550, Application US/09826509
; Publication No. US20030204073A1
; GENERAL INFORMATION:
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: No. US20030204073A1-Endogenous, Constitutively Activated Known G
; TITLE OF INVENTION: Protein-Coupled Receptors
; FILE REFERENCE: AREN-207
; CURRENT APPLICATION NUMBER: US/09/826,509
; CURRENT FILING DATE: 2001-04-05

; PRIOR APPLICATION NUMBER: 60/195,747
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 589
; SOFTWARE: PatentIn Version 2.1
; SEQ ID NO 550
; LENGTH: 1335
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-826-509-550

Query Match 45.7%; Score 507; DB 11; Length 1335;
Best Local Similarity 69.7%; Pred. No. 1.1e-132;
Matches 703; Conservative 0; Mismatches 300; Indels 6; Gaps 1;

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Qy         80 ATGAAGATGAGTTTCTCCGCTATCTGTGGCGTGATTATCTGTACCCAAAACAGTATGAGT 139
              | || || || || || || || |||||| | || || ||| |||| ||| | |||||||
Db        104 ACGACGAGGAATTCCTGCGGTACCTGTGGAGGGAATACCTGCACCCGAAAGAATATGAGT 163

Qy        140 GGGTCCTCATCGCAGCCTATGTGGCTGTGTTCGTCGTGGCCCTGGTGGGCAACACGCTGG 199
              ||||||| ||||| |  ||  |    |||||||||||||| ||  | || |||   ||||
Db        164 GGGTCCTGATCGCCGGGTACATCATCGTGTTCGTCGTGGCTCTCATTGGGAACGTCCTGG 223

Qy        200 TCTGCCTGGCCGTGTGGCGGAACCACCACATGAGGACAGTCACCAACTACTTCATTGTCA 259
              | ||  |||| ||||||  |||||||||||||||||| || ||||||||||||| ||||
Db        224 TTTGTGTGGCAGTGTGGAAGAACCACCACATGAGGACGGTAACCAACTACTTCATAGTCA 283

Qy        260 ACCTGTCCCTGGCTGACGTTCTGGTGACTGCTATCTGCCTGCCGGCCAGCCTGCTGGTGG 319
              | || || |||||||| || || |||||    | |||||| || ||||  ||| | ||||
Db        284 ATCTTTCTCTGGCTGATGTGCTCGTGACCATCACCTGCCTTCCAGCCACACTGGTCGTGG 343

Qy        320 ACATCACTGAGTCCTGGCTGTTCGGCCATGCCCTCTGCAAGGTCATCCCCTATCTACAGG 379
              | ||||||||| ||||| | || || ||  |||| ||||| || || || |||||||||
Db        344 ATATCACTGAGACCTGGTTTTTTGGACAGTCCCTTTGCAAAGTGATTCCTTATCTACAGA 403

Qy        380 CTGTGTCCGTGTCAGTGGCAGTGCTAACTCTCAGCTTCATCCCCCTGGACCGCTGGTATG 439
              | ||||| ||||| ||| | || || || || ||||  ||| || |||| || |||||||
Db        404 CCGTGTCGGTGTCTGTGTCTGTCCTCACACTGAGCTGTATCGCCTTGGATCGGTGGTATG 463

Qy        440 CCATCTGCCACCCACTATTGTTCAAGAGCACAGCCCGGCGGGCCCGTGGCTCCATCCTGG 499
              | ||||| |||||  |  |||| ||||||||||   |||||||||  |  |||  |
Db        464 CAATCTGTCACCCTTTGATGTTTAAGAGCACAGCAAAGCGGGCCCGTAACAGCATTGTCA 523

Qy        500 GCATCTGGGCTGTGTCGCTGGCCATCATGGTGCCCCAGGCTGCAGTCATGCAATCCAGCA 559
              |||||||  ||| ||       || ||| | || |||||    ||||||  | |||||
Db        524 TCATCTGGATTGTCTCCTGCATTATAATGATTCCTCAGGCCATCGTCATGGAGTGCAGCA 583

Qy        560 GTGTGCTGCCTGAGCTAGCCAACCGCACACGGCTCTTCTCACTCTGTCATGAACGCTGGG 619
                ||| | || |   |||||||    ||    |||||  |  | ||| |||| |||||||
Db        584 CCGTGTTCCCAGGCTTAGCCAATAAAACCACCCTCTTTACGGTGTGTGATGAGCGCTGGG 643

Qy        620 CAGATGACCTCTATCCCAAGATCTACCACAGTTGCTTCTTTATTGTCACCTACCTGGCCC 679
              | |||  | |||||||||| |||||||  || ||||||  | || || ||| |||| |
Db        644 GTGGTGAAATTTATCCCAAGATGTACCACATCTGTTTCTTTCTGGTGACATACATGGCAC 703

Qy        680 CACTGGGCCTCATGGCCATGGCCTATTTCCAGATATTCCGCAAGCTCTGGGGCCGCCAGA 739
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Db        704 CACTGTGTCTCATGGTGTTGGCTTATCTGCAAATATTTCGCAAACTCTGGTGTCGACAGA 763

Qy        740 TCCCCGGCACCACCTCAGCACTGGTGCGGAACTGGAAGCGCCCCTCAGACCAGCTGGGGG 799
                ||||  ||  ||   |  ||  |  |  |    |  |  ||  |||||||  ||         ||||   |
Db        764 TCCCTGGAACATCATCTGTAGTTCAGAGAAAATGGAAGCCCC------TGCAGCCTGTTT 817

Qy        800 ACCTGGAGCAGGGCCTGAGTGGAGAGCCCCAGCCCCGGGGCCGCGCCTTCCTGGCTGAAG 859
                  |  |    |   ||  |    |          |   ||  |||||     ||||   |    |||||||
Db        818 CACAGCCTCGAGGGCCAGGACAGCCAACGAAGTCCCGGATGAGCGCTGTGGCGGCTGAAA 877

Qy        860 TGAAGCAGATGCGTGCACGGAGGAAGACAGCCAAGATGCTGATGGTGGTGCTGCTGGTCT 919
                |  ||||||||  ||  ||   |  |||||  |||      ||||  |||||||  |||||   ||||  |
Db        878 TAAAGCAGATCCGAGCCAGAAGGAAAACAAAACGGATGTTGATGGTTGTGCTTTTGGTAT 937

Qy        920 TCGCCCTCTGCTACCTCCCCATCAGCGTCCTCAATGTCCTTAAGAGGGTGTTCGGGATGT 979
                |  ||   |  |||||  ||  ||  ||  |||  ||||||||||  ||  |||||  ||  ||  |||||||
Db        938 TTGCAATTTGCTATCTACCAATTAGCATCCTCAATGTGCTAAAGAGAGTATTTGGGATGT 997

Qy        980 TCCGCCAAGCCAGTGACCGCGAAGCTGTCTACGCCTGCTTCACCTTCTCCCACTGGCTGG 1039
                |    |||   |     |||  |  ||   ||||  ||  |||||  ||  |||||  ||  ||||||||  |
Db        998 TTGCCCATACTGAAGACAGAGAGACTGTGTATGCCTGGTTTACCTTTTCACACTGGCTTG 1057

Qy       1040 TGTACGCCAACAGCGCTGCCAACCCCATCATCTACAACTTCCTCAGTGG 1088
                |  ||  |||||  ||  |||||  ||  ||  ||  ||  ||  ||  ||||||||
Db       1058 TATATGCCAATAGTGCTGCGAATCCAATTATTTATAATTTTCTCAGTGG 1106
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Job time : 575.496 secs